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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title: US-09-455-486-6
Perfect score: 2351
Sequence: 1 MESISNMGSPKSLSETCLPN.....ALVLPSIVILDLLQLCRYPD 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
A Geneseq_29Jan04:*
1: geneseqp1990s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003s:*
6: geneseqp2003bs:*
8: geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                March 1, 2004, 19:53:00 ; Search time 96 Seconds
(without alignments)
1336.214 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                           1586107 seqs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compagen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                1586107
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	Bd	ID		
1	2351	100.0	454	44	AAE02781	Aae02781 Human six	
2	2351	100.0	454	4.	AAU10188	8 Human C	
ω	2351	00.	454	W	ABG61933	Abg61933 Prostate	
4	2351	100.0	454	ហ	AAU76538	ш	
υī	2351	00	454	υ	AAU80190	Aau80190 Human PUM	
σ	2351	00.	454	7	ABU08893	Abu08893 Tumour-as	
7	2348		454	7	ADB65001	Human	
œ	2294		490	ທ	AAE28951	Aae28951 Human STE	
9	2294		490	7	ABU63312	Human	
10	2290		490	4.	AAU10187	Human	
11	2036		419	A	AAU10189	Human	
12	1972.5		576	4.	ABG12306		
13	1972.5		1273	4,	ABG00113	Abg00113 Novel hum	
14	1738	73.	450	4	AAE02841		
15	1364.5	83	1082	σ	ABP62883	_	
16	1316	56	488	4	AAB49483		
17	1316	56.	526	ω	ABB83365		
18	1272	54	488	42	AAB85775	Human	
19	1272	54	488	ហ	ABB83366	Abb83366 Human Tum	
20	1269	54	488	4	AAB93224	Aab93224 Human pro	
21	1269	ت 4	488	4.	AAU04564	Human	
22	1269	54	488	4.	AAU10220	Human	
23	1269	54	488	σ	ABU60864	Human	
24	1245.5	53.0	487	4.	AAB49481	Aab49481 Human p-H	
25	1088	4	459	4	AAB74715	Aab74715 Human mem	

WO200140276-A2.

07-JUN-2001.

45	44	43	42	41	40	39	38	37	36	ω S	ω 4	ω W	32	31	30	29	28	27	26
717	736	768	768	844	844	844	844	844	844	844	844	844	844	901	1074.5	1082	1085	1087	1087
•	31.3	32.7	32.7	35.9	35.9	35.9	35.9	35,9	35.9	35.9	35.9	35.9	35.9	38.3	45.7	46.0	ð	σ	46.2
267	141	237	237	179	179	179	179	179	179	179	179	179	179	173	456	458	459	459	459
o,	w	σ	4.	σı	4	4	4,	4	4	4	4	4.	4	W	4	4.	4	ຫ	4
ABU60886	AAY52589	ABU60865	AAU04565	ABG39817	AAM05646	ABG51883	AAM57768	AAM70183	ABB22356	ABB31810	AAM30517	ABB37041	AAM18006	AAY58195	AAB49482	AAE02636	AAU10190	ABP64820	AAE02782
Abu60886	Aay52589	Abu60865	Aau04565	Abg39817	Aam05646	Abg51883	Aam57768	Aam70183	Abb22356	Abb31810	Aam30517	Abb37041	Aam18006	Aay58195	Aab49482	Aae02636	Aau10190	Abp64820	Aae02782
Human G	Human pro	Human G p	Human G	Human pep	Peptide #	Human 1	Human bra	Human bon	Protein	Peptide	Peptide	Peptide	Peptide	Human STR	Human p-H	Human STE	Human	Human	Human six

ALIGNMENTS

RESULT 1	LT 1 2781	
: 5	02781	standard; protein; 454 AA.
AC X	AAE02781;	
×		
X H	06-AUG-2001 (f	(first entry)
X D	Human six trans	transmembrane epithelial antigen of prostate (STEAP)-2 protein.
Ş	Human; cytostat	
XX.	six transmembra	six transmembrane epithelial antigen of the prostate-2; STEAP-2;
KW	chromosome 7q21;	
Κ¥		,
×	-	
20	Homo sapiens.	
×		
문	Key	(1
9 1	Region	ייייייייייייייייייייייייייייייייייי
H .	Region	153 165
FT		/label= Immunogenic_peptide #1
FΤ	Domain	28
₽Τ		/label= Transmembrane_domain #1
1 4	Region	
1 m	Domain in)55 277 255 277
H 7		/label= Transmembrane domain #2
FT	Domain	
FΤ		/label= Transmembrane_domain #3
FΤ	Region	14
FT		/label= HLA-A2_binding_peptide #4
FT	Region	
FT		/label= HLA-A2_binding_peptide #3
L	Region	345, .358
ΤŢ		/label= Immunogenic_peptide #2
H H	Domain	(1) b) Herrison brown by the second
1 7	7	ranswellanc and actual
#1 # #1 #	Company	/label= Transmembrane domain #5
Į,	Region	
ĦŢ	(/label= HLA-A2_binding_peptide #2
FT	Domain	428450
\$ 'P		/label= Transmembrane_domain #6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP) -2 protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP 2 gene is located on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP protein with a cancer that expresses STEAP, or in a patient, comprises administering a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expresses STEAP, or comprises the variable domains of the heavy and light chain is for the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody coding that the vaccional antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody coding antibody is expressed intracellularly. Note: This sequence is stated to be the same as that being shown as SEQ ID NO:8 (AABC2841) in sequence listing of the specification. However both the sequences differ at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 454
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DB; AAD07072.
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                                                                                                                                                                                                                                                                                                                                  RINGYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE
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                                                                                                                                                                                                                                                         LARQLNFI PIDLGSLSSAREIENL PLRL FTLWRGPVVVAISLAT FFFLYS FVRDVIHPYA
                                                                                                                                                                                                                                                                                                   RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE
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                                                                                                                                                                                                                                                                                                                                                                                                    RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM
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 EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
                                                                                                 CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMY
                                                                                                                                 CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANI ENSWNEEEVWRI EMY
                                                                                                                                                                  RNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ
                                                                                                                                                                                                                                  LARQUNFIPIDLGSUSSAREIBNUPURLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA
                                ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
                                                       ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epithelial antigen of the prostate) cancers, useful for detecting and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2351; DB 4;
Pred. No. 5e-245;
); Mismatches 0;
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EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD
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Human ORF2
                                                                                       16-JAN-2002
                                                                                          AAU10188;
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                                                                                                88 2
                                                                                              standard;
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fi
                                                                                       (first
                                                                                   Six-Transmembrane Protein
                                                                                              protein;
                                                                                       entry)
                                                                                              454
                                                                                   of.
                                                                                   Prostate
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Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate can benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lympholeukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancliver cancer; lung cancer; cytostatic; ORF2.

Homo sapiens.

WO200172962-A2

23-MAR-2001; 2001WO-US009410.

24-MAR-2000; 2000US-0191929P

(SAAT/) SAATCIOGLU

2001-662926/76. DB; AAS15810, AAS15811.

New polynucleotide for the diagnosis, prevention and treatment prostate and testis disorders, particularly prostate cancer, coprostate-specific or testis-specific nucleic acids. comprises

Claim 1; Fig 4H; 114pp; English.

The invention relates to substantially pure prostate-specific or testisCC specific polypeptides and the nucleic acids encoding them. Also included
CC are vectors and host cells expressing the proteins, a transgenic animal
CC expressing the protein, antibodies against the proteins, probes for
CC detecting the nucleic acids, antisense molecules for the nucleic acids
CC and methods of isolating modulators of the proteins. Compounds that
CC modulate the prostate specific or testis specific polypeptide are useful
CC to diagnose, prevent or treat disorders of the testis or prostate
CC prostatilis, testicular cancer, cryptorchidism, undescended, retractile,
CC ascending or vanished testis. Other proliferative disorders for which the
CC accer, breast cancer, pancreatic cancer, liver cancer and lung cancer.
CC The present sequence is prostate specific protein, Six-Transmembrane
CC Protein of Prostate 1, STMP1, ORF2

Sequence 454 A

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Best Local S
Matches 454
                                                                                              454;
61
                      61
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             RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM
                                                             MESISM/GSPXSLSETCLFNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS
                                                MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS
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ilarity 100.0%;
Conservative (
                                                                                              0
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Pred. No. 5e-245;
Mismatches 0;
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AND ABG61933

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24-JAN-2001;
16-MAR-2001;
16-MAR-2001;
06-APR-2001;
24-APR-2001;
30-APR-2001;
The present invention relates to methods of detecting a prostate cancer-
associated transcript in a cell from a patient. The method comprises
contacting a biological sample from the patient with prostate cancer-
                                                                                                                                                                                                                                                                                                                          Gish
                                                                                                                                                           Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC by determining if prostate cancer-associated genes are expressed in a
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DB; ABK92252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABG61800-ABG61944 represent prostate cancer-associated proteins
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Similarity 100.0%;
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EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD
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Pred. No. 5e-245;
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AAU76538 standard; protein; 454 ₽

05-JUN-2002 (first entry)

Tumour-associated antigenic target protein, TAT138

TAT138; Tumour-associated Antigenic Target; tun colorectal cancer; lung cancer; ovarian cancer; central nervous system cancer; liver cancer; bl Modified-site Homo pancreatic sapiens nervous system tic cancer; leu! <u>დ</u> Location/Qualifiers leukaemia; "N-myristoylation gene therapy tumour; bladder breast cancer; cancer; melanoma;

Modified-site

/note= 24. .29

site"

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The invention relates to an isolated tumour-associated antigenic target colypeptide (TAT) (I), specifically TAT134 TAT138 polypeptides, and the polypucleotides (II) encoding them. (II) is useful for diagnosing the presence of a tumour in a mammal, where the level of expression of (II) is indicative on the presence of tumour in the mammal from which the test sample was obtained. Antibody to (I) is useful for killing a cancer cell, sample was obtained. Antibody to (I) is useful for killing a cancer cell, a colorect all cancer cell, a lung cancer cell, a novarian cancer cell, a central nervous system (CNS) cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a colliver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a colliponucleotide probes or for encoding fragments of full length TAT colliponucleotide probes or for encoding fragments of full length TAT colliponucleotide probes or for encoding fragments of full length TAT colliponucleotide probes for mapping the gene encoding TAT and for genetic canalysis of individuals with genetic disorders. (II) is also useful for generating either transgenic animals or knockout animals, and in gene therapy. The TAT polypeptides and nucleic acids may also be used for tissue typing and the TAT polypeptides are useful for staging TAT collypeptide (agonist) or prevent the effect of TAT collypeptide (agonist) or prevent the effect of TAT collypeptide (agonist) is useful for staging TAT
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Wood WI,
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01-DEC-2000;
28-FEB-2001;
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29. .32
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phosphorylation site"
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Matches 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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RNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ
                                       RNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ
                                                                                  LAROLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA
                                                                                                                                                                     RINGYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE
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Pred. No. 5e-245;
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The invention discloses human nucleic acids encoding tumour-associated antigenic target (TAT) polypeptides, with or without their associated signal peptide. Also disclosed is an antibody that specifically binds to the TAT polypeptides, a method for detecting the presence of a tumour in a mammal and a method for killing a cancer cell expressing the TAT polypeptide. The nucleotide sequences are useful in preparing TAT polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The TAT polypeptides are useful as therapeutic agents and for detecting the presence, prevention and/or treatment of a tumour, such as colon, breast or prostate tumour. The TAT polypeptides and nucleic acids may also be used diagnostically for tissue

Claim 12; Fig

10; 71pp; treating

diagnosing

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New nucleic acid, useful for the manufacture

tumor English.

in a mammal.

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medicament

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Wood WI,
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24-AUG-2000;
26-SEP-2000;
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02-JUN-1999;
01-SEP-1999;
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17-JUN-1998;
10-SEP-1998;
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02-MAR-2000;
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u TD, Zha
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99WO-US020111
2000WO-US004341
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2000WO-US008439
2000WO-US0233451P
2000WO-US0233451P
2000WO-US035678
2000WO-US006666
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98US-0089653P.
98US-0099792P.
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Best Local
Isogai T,
Yamamoto J
Seki N, Y
                                                                                                                                                      05-NOV-2001;
25-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                        transcription-related cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
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RES ASSOC
Yoshikawa T,
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Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, N
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WPI; 2003-450961/43 N-PSDB; ADB63031.

New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or of gene therapy.

Claim 1; Page; 222pp; English.

The invention discloses a polynucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polypucleotide CC or its partial peptide, an antibody binding to the polypeptide or peptide CC of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide CC with the antibody of the encoded protein, and observing the binding CC between the two, a transformant carrying the polynucleotide in an CC expressible manner and an antisense polynucleotide. The oligonucleotide carposesible manner and an antisense polynucleotide, or as a probe CC for detecting the polynucleotide. The polynucleotide, or as a probe CC for detecting the polynucleotide. The polynucleotide and encoded CC genes may be included in them, for developing a diagnostic marker or CC medicines for regulation of their expression and activity, or as targets CC gene therapy. The genes are involved in tissue and/or cell CC transcription-related proteins, signal transduction-related proteins, CC transcription-related proteins, disease-related proteins and genes cencoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate CC sequence presented is a protein of the encoded protein to treat diseases. The sequence data for this patent is not represented in the printed by the sequence data for this patent is not represented in the printed by the European Patent Office.

Sequence 454 Š

Length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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cc useful for detecting expression of the protein in a sample, where the sample is lung or prostate tissue sample and the protein is diagnostic differentially expressed when compared with a standard and is diagnostic confaring everal molecules and compounds to identify an antibody that specifically binds the protein. The protein is useful for coreening several molecules and compounds to identify at least one ligand. The protein is also useful for preparing and purifying a polyclonal antibody and for preparing a monoclonal antibody using standard animal immunisation/hybridoma methods. A TMPL specific antibody is useful to detect expression of the protein in a lung or prostate tissue sample and the method is useful as a diagnostic for lung or prostate cancer. A TMPL specific antibody is also useful for immunopurifying a protein, for treating a prostate cancer and for delivering a therapeutic agent to a cancer, preferably prostate cancer. The protein is useful for diagnosing, staging, treating or monitoring progression or treatment of cancer, preferably lung or prostate cancer. The present sequence represents the amino acid sequence of the human
                                                                                                                                                                                                                                                                                                                                                                                  New transmembrane protein differentially expressed in prostate and tumors, useful for diagnosing, staging, treating or monitoring progression or treatment of cancer, preferably lung or prostate can
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99US-00397558.
2001US-00802520.
2001US-00963896.
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Pred. No. 8.4e-239;
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CC specific polypeptides and the nucleic acids encoding them. Also included
CR are vectors and host cells expressing the proteins, a transgenic animal
CR expressing the protein, antibodies against the proteins, probes for
CR detecting the nucleic acids, antieense molecules for the nucleic acids
CR and methods of isolating modulators of the proteins. Compounds that
CR condulate the prostate specific or testis specific polypeptide are useful
CR to diagnose, prevent or treat disorders of the testis or prostate
CR controllarly prostate cancer, benign prostatic hyperplasia, acute
CR controllarly prostate cancer, benign prostatic hyperplasia, acute
CR controllarly or vanished testis. Other proliferative disorders for which the
CR cancer, breast cancer, pancreatic cancer, leukaemia, melanoma, ovarian
CR cancer, breast cancer, pancreatic cancer, leukaemia, melanoma, ovarian
CR cresent sequence represents a prostate specific protein, Six-
CR Transmembrane Protein of Prostate 1, STM,1
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DB; AAS15793, AAS15801,
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                                                                       RNQQSDFYKIPIBIVNKTLPIVAITLLSLVYLAGLLLAAAYQLYYGTKYRRFPPWLETWLQ
                                              RNOOSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYOLYYGTKYRRFPPWLETWLO
                                                                                                                     LARQLNFIPIDLGSLSSAREIENLPLRLFTFWRGPVVVAISLATFFFLYSFVRDVIHPYA
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Pred. No. 2.3e-238;
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CC specific polypeptides and the nucleic acids encoding them. Also included
CC are vectors and host cells expressing the proteins, a transgenic animal
CC expressing the protein, antibodies against the proteins, probes for
CC detecting the nucleic acids, antisense molecules for the nucleic acids
CC and methods of isolating modulators of the proteins. Compounds that
CC to diagnose, prevent or treat disorders of the testis or prostate
CC particularly prostate cancer, benign prostatic hyperplasia, acute
CC prostaticis, testicular cancer, cryptorchidism, undescended, retractile,
CC ascending or vanished testis. Other proliferative disorders for which the
CC modulators may be used include lymphoma, leukaemia, melanoma, ovarian
CC cancer, breast cancer, pancreatic cancer, leukaemia, melanoma, ovarian
CC The present sequence is prostate specific protein, Six-Transmembrane
CC Protein of Prostate 1, STM;1, ORF3
                                                                                                                                                                                                                                                    Query Match
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Matches 394
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                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                            Local
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                                              RNPXFASBFFPHVVDVTHHBDALTKTNIIFVAIHRBHYTSLWDLRHLLVGKILIDVSNNM
                                                                                                                                                                          MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 4K; 114pp; English.
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RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM
                                                                                                                           MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS
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Pred. No. 5.5e-211;
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sequences. (I) is useful as hybridisation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed cC genes. (I) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a polyment. (II) and its binding partners are useful for medical imaging CC of sites expressing (II). (I) and (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The CC polypeptide and polymucleotide sequences have applications in
                    RESULT 12
ABG12306
ID ABG12306
ID ABG12
XX ABG12
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XW Homo
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XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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Best Local Similarity
Matches 390; Conser
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                                                                            31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
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2000US-00649167.
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87.4%;
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Pred. No. 6.7e
0; Mismatches
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.7e-204;
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PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AA664300.

XX New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations production professity.

YX New isolated polynucleotide and encoded polynucleotide (I) and polypeptide (II) diagnostics, forensics, gene mapping, identification of mutations production professity.

XX Claim 20; SEQ ID NO 30472; 103pp; English.

XX Claim 20; SEQ ID NO 30472; 103pp; English.

XX Claim 20; SEQ ID NO 30472; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, coligomers, and for chromeome and gene mapping, can din recombinant production of (II). The polynucleotides are also used genes. (I) is useful in gene therapy techniques to restore normal cartivity of (II) or to treat disease states involving expressed genes. (I) is useful in gene therapy techniques to restore normal capturer of (II) or to to treat disease states involving of (II). (II) is useful for generating antibodies against it, detecting or quantitating a cuplement. (II) and tis binding partners are useful in medical imaging complement. (II) and tis binding partners are useful in medical imaging complement of the protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in collapostics, forensics, gene mapping, identification of mutations responsible for genetic dissorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and can decide sequences. ABG00010-ABG03077 represent novel human diagnostic captured format diagnostic captured format diagnostic captured format diagnostic captured by the product dependent on DNA and captured format diagnostic captured by the sequence of the invention. Note: The sequence data for this general profess of the invention of the product data for this general profess of
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30 Sequence 1273 AA;

Query Match

83.9%; Score 1972.5; DB 4; Length 1273;

Best Local Similarity 87.4%; Pred. No. 2.3e-203;

Matches 390; Conservative 0; Mismatches 1; Indels 55; Gaps

421 373 313 241 181 193 133 412 361 301 253 121 61 73 ы CRKOI LARQLNFIPIDLGSLSSARBIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA RINGYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASROVYICSNNIQARQQVIE RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNWAYQQVHANIENSWNEEEVWRIEMY RNOOSDEYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRREPPWLETWLQ LARQUNFIPIDLGSLSSARBIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM MESISMMGSPKSLSETFLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS EEYYRFYTPPNFVLALVLPSIVILDL ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE RNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ Conservative LGLLSFFFAMVHVAYSLCLPMRRSBRYLFLNMAYQ 0; 446 OSTLGYVALLISTFHVLIYGWKRAFE Indels ភ ភ 240 360 300 312 252 180 192 120 132 9 411

5

438

463

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RESULT 14
AAE02841
ID AAE02
located on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient, comprises administering a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody is expressed intracellularly. Note: This sequence is stated to be the same as that being shown as SEQ ID NO:8 (AREO.781) in figure 9A-9C
Sequence
                                                                                                                                                                                                                                     The present sequence is an alternative version of human six transmembrane epithelial antigen of the prostate (STEAP)-2 protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is
                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                    proteins,
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                        e specification. However the present sequence lacks several amino at its N-terminal end and has additional amino acids at its C-nal end when compared with the sequence shown in figure 9A-9C
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                                                                                                                                                                                                                                                                                             Page 175-176; 187pp; English.
                                                                                                                                                                                                                                                                                                                                    expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                    Jakobovits
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embrane epithelial antigen of the prostate-2; STEAP-2;
7q21; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                                                                                                                                                                                                                                                               Hubert RS,
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RESULT 15
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Matches
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                                                                                                                                                                                                                                                                                                                                                                   Human; vulnerary; dermatological; neuroprotective; nootropic; ca
antiparkinsonian; immunostimulant; cytostatic; immunosuppressive
antidiabetic; antiallergic; gene therapy; wound healing; tissue
burn; central nervous system disorder; Alzheimer's disease;
                                                                                                                     WPI; 2002-583321/62.
N-PSDB; ABQ93362.
                                                                                                                                                                                                                                              31-AUG-2001; 2001WO-US027093
                                                                                                                                                                                                                                                                                                                                              Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
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                                                                                                                                                                                                (HYSE-)
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                                                        w polynucleotide and polypeptides, useful for treatment and diagnosis Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral elevosis, immune deficiencies, cancer, autoimmune disorders, multiple elerosis, diabetes and allergies.
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                                                                                                                                                       Asundi V,
Wang D, 1
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                                                                                                                                                                                                                                                                                                                                                                                            dermatological; neuroprotective; nootropic; can immunostimulant; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO
                                                                                                                                                         Liu
                                                                                                                                                        Zhou
iu C,
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                                                                                                                                                        Xue AJ,
manac RT,
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Pred. No. 1.1e-178;
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Wehrman
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n T;
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sclerosis,

Claim 20; SEQ ID NO 320; 284pp + Sequence Listing; English.

invention relates to an isolate sequences (ABQ93288-ABQ93532).

isolated polynucleotide (I)

Treating

a condition

comprising comprising

one

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Query Match
Best Local Similarity 83.2
Matches 272; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1082 AA;
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246 EEEYYRFYTEPNEVLALVLESIVILDL 272
                                       420 EEEYYRFYTPPNFVLALVLPSIVILDL 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.0%; Score 1364.5; DB 5; Length 1082; 83.2%; Pred. No. 1.1e-137; Vative 0; Mismatches 0; Indels 55;
                                                                                                                                            OSTLGYVALLISTFHVLIYGWKRAF 245
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Search completed: March 1, 2004, 23:33:05 Job time: 102 secs

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Minimum DB seq length: 0
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Perfect score:
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                             Scoring table:
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PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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2351
1 MESISMMGSPKSLSETCLPN.....ALVLPSIVILDLLQLCRYPD 454
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C71391	AF2479	A28439	C71219	A85045	T11181	A83006	C86250	T02134	F69144	T12284	E71139	T41068	AG3547	T39453	H98310
NADH2 dehydrogenas	ABC transporter AT	endonuclease Scel	hypothetical prote	probable glucan sy	NADH2 dehydrogenas	hypothetical prote	hypothetical prote	n	O-antigen transpor	NADH2 dehydrogenas	hypothetical prote	hypothetical prote	bicyclomycin resis	probable mrna stab	probable peptide A

ALIGNMENTS

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Appothetical protein alr8074 [imported] - Nostoc sp. (strain PCC 7120) plasmid C.Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AC2560

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable oxidoreductase [imported] - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000 C;Accession: T50571
R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kina-R;Redenbach, M.; Kieser, H.M.; Denapaite, D.;
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C; Superfamily:
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A;Title: A set of ordered cosmids and a detailed genetic and
A;Reference number: Z20556; MUID:97000351; PMID:8843436
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A; Genome: plasmid
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A; Residues: 1-239 < RED>
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A;Molecule type: DNA
A;Residues: 1-211 <KUR>
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T50571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from
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Best Local S
Matches 61
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   83
                                                          81 DALTKTNIIFVAIHRE-HYTSLWDLRHLLVGKILIDVSNNMRINQ-----YPE--SNAE 131
                                                                                                                                       23
                                                                                                                                                                                                                                                                               61;
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                                                                                                                                                                                                         25 IKDARKVTVGVI-GSGDFAKSLTIRLIRCGYHVVIGSR---NPKFASEFFPHVVDVTHHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 IAFIGIGQVGSALASQLLSLDHTVTIAARNSNSDSVKTALAKYPE-LQVSSPQEAIAQAE
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ETARRSDVVIVAVPWDGHGKTLESLRAELSGKLVVDCVNPLGFDKKGAYALKPEEGSAAE 142
                                                                                                                                   LPDVSGLVVGVLGGTGPQGKGLAYRLAKAGQKVIVGSRAAERAAAAEEIGHGVEGADNA
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                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein MJ1501
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi,
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                                                                                                                                                                                                                                                                    6.7%; Score 156.5; DB
27.9%; Pred. No. 5e-05;
tive 41; Mismatches
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Pred. No. 2.4e-05;
3; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:CAB61708.1
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, M.; Yasuda, M.;
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Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Wosse, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch: A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: H69400
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Conserved hypothetical protein AF1209 - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
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A;Residues: 1-213 <KLE>
A;Residues: 1-213 <KLE>
A;Cross-references: GB:AE001021; GB:AE000782; NID:g2689344; PIDN:AAB90038.1; PID:g26493
C;Superfamily: conserved hypothetical protein MJ1501
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Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness,
lodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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90, 364-370, 1997
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DLGSLSSAREIENL-PLRLFTLWR
                                                                         KLASVLEESSVVAAYHSIPARRFANLGEEFEWDVPICGDS-GAKEVVVDLTEKISGLRAL
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irkness, E.F
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to

RESULT D69361

conserved hypothetical protein AF0892 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Date: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999 Accession: D69361

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.T.; Artiach, P.; Kaine, B.P.; Sykes, A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae(A,Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: D69361 A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA A;Residues: 1-212 <KLE> A;Residues: 1-212 <KLE> A;Residues: 1-212 <KLE> A;Cross-references: GB:AE001042; GB:AE000782; NID:g2689365; PIDN:AAB90348.1; PID:g26497(C;Superfamily: conserved hypothetical protein MJ1501

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T10120
F420-dependent NADP 1
C;Species: Methanobac
C;Species: 16-Jul-1999 #
C;Accession: T10120
C;Accession: T10120
C;Beck, H.; Thauer; R
hypothetical protein MJ1501 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep_1996 #sequence_revision 13-Sep_1996 #text_change 21-Jul-2000 C;Accession: D64487
C;Accession: D64487
C;Cotcosion: Methanococcus Jannas M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
C;Cotcosion: M.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
C;Cotcosion: M.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
C;Cotcosion: M.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Fraser, C.M.; Smith, H.O.; Woese
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaso
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A;Title: F420H2:NADP oxidoreductase from Methanobacterium thermoautotrophicum:
A;Reference number: 216959; MUID:99037734; PMID:9821972
A;Accession: T10120
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                                                                                                                                                                                                                                         IDCGGLENARVIEKITPLLINL
                                                                                                                                                                                                                                                                         IDLGSLSSAREIENLPLRLFTL
                                                                                                                                                                                                                                                                                                         RFLEDQGTRVAAAFNNISASALLDITGPVDC--DCLIASDHRDALDLASELAEKIDGVRA 184
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Pred. No. 0.00
44; Mismatches
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Pred. No.
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 Fraser, C.M.; Smith, H.O.; Woese, c archaeon, Methanococcus jannaschi
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A; Residues: 1-191 <STO>
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47; Conserv
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: F86826
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A; Cross-references: GB:U67591;
C; Genetics:
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A;Accession: D64487
A;Status: preliminary; nucleic acid sequence not shown;
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Cross-references: GB:AB005176; PID:g12724621; PIDN:AAK05712.1; GSPDB:GN00146;Experimental source: strain IL1403
                                          190 IDLGSLSSAREIENLPLRLFTL-----WRG
                                                                                    AKQLPNSMIVKAFN--TTFSDTLATKKVANEHQTTVLLASDSQEAKETIIKALENSGLSL
                                                                                                                                                                           VVLAVPYVAIAGIIQEYSTD-----LQGKIIIDITNPVDFTTFDSLLVPSDTSAAALI
                                                                                                                                                                                                                                                                                                          TVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTKTN----
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LDAGSLKRARELEAIGFLQITLAASEKISWDG
                                                                                                                               ASLFFDSLIVKGFNVVSAWALQLGPKDASRQ----VYICSNNIQARQQVIELARQLNFIP
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Pred. No. 0.0033;
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A;Reference number: Z14115; MUID:98332717; PMID:9666070
A;Accession: T00121
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-216 <TAK>
A;Residues: 1-216 <TAK>
A;Cross-references: EMBL:AB010203; NID:92780763; PIDN:BAA24368.1; PID:92780765
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A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu: A;Reference number: A69000; MUID:98037514; PMID:9371463
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Gene 215, 37-45, 1998
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C;Superfamily:
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                                             VLCSKGSVASEVLTLSGIDSLNGKTIIDTTNPISEIPPQNGVLNFFTSYNESLMEKLQKQ 125
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  FPDSLIVKGFNVVSAWALQLGP--KDASRQVYICSNNIQARQQVIELARQLNFIPIDLGS 194
                                                                                                                                              IGILGSGIVGQTLANGFLKYGAEVKIGTRDFGKLKDWLAKAGAGASIGSFSEAANFGEII
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23.7%; Pred. No. 0.0:
tive 37; Mismatches
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23.8%; Pred. No. 0.0
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 C;Accession: AB3182 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Cerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Ku; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
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AB3182
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A;Molecule type: DNA
A;Residues: 1-242 <SIM>
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R;anonymous, The Xyle
Nature 406, 151-157,
                                                                                                                                            conserved hypothetical protein Atu5183 [imported] -
C;Species: Agrobacterium tumefaciens
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A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
Briones, Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marxino, C.L.; Marques, M.V.; Marcins,
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Nosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M., Silva Jr., W.A.; da Silva
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
A;Authors: da Silva, A.S.; Vettore, A.L.;
A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The genome sequence of the plant pathogen Kylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 bel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein XF1737 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa (Strain C;Species: Xylella fastidiosa (S;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AE003997; GB:AE003849; NID:g9106805; PIDN:AAF84546.1; GSPDB:GN00;
149 YMPGARLVRAFSAVDATVVE---TSASRRGGRIGMPLASDDAEAMKVAEGLVRDAGCDPV
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                                                                                                                                                                                                                                                                                                               84 TKTNIIFVAIHREHYTSLW-DLRHLLVGKILIDVSNNMRINQ---YPESN----AEYLAS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 ARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNP----KFASEFFPHVVDVTHHEDAL
                                                                                                        LFPDSLIVKGFNVVSAWALQLGPKDASRQ-----VYICSNNIQARQQVIELARQLNFIPI
                                                                                                                                                                                                                 EFGTVLLLAVPFEALPQVGRDLRSAYRGKIVLDSTNPWGASSADVYREARELGVAQTVVK
                                                                                                                                                                                                                                                                                                                                                                                                                        AAPMRIGVIGAGSLGGTVGRLWVKAGHEVMFSSRNPDKLEAMARELEPR-ASVGQPLAAT
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           205
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; Chen, L.; Wood, G.E.; Chen, Kutyavin, T.; Levy, R.; Li, I

#text_change 18-Nov-2002

Agrobacterium

tumefaciens

(strain

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F;399-421/Domain: transmembrane #s
F;444-465/Domain: transmembrane #s
F;486-508/Domain: transmembrane #s
F;529-550/Domain: transmembrane #s
F;529-550/Domain: transmembrane #s
F;509-630/Domain: transmembrane #s
F;609-630/Domain: transmembrane #s
F;191,199,293,318/Binding site: #s
F;191,199,293,316/Binding site: #s
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A; Residues: 1-198 < KUR>
A; Residues: 1-198 < KUR>
A; Cross-references: GB: AE008687; PIDN: AAL45872.1;
A; Cross-references: strain C58 (Dupont)
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AB3182
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X74454; NID:g396801; PII A;Note: the authors translated the codon AGT for C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      follitropin receptor precursor - crab-eating macaque N,Alternate names: follicle-stimulating hormone receptor (FSHR) C;Species: Macaca fascicularis (crab-eating macaque) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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A; Residues: 1-695 < GRO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycopy; Superfamily: glycoprotein hormone receptor; physoprotein; hormone receptor; physoprotein; hormone receptor; physoprotein; signal sequence #status predicted <SIG>1-17/Domain: signal sequence #status predicted <PFH>1-1-17/Domain: signal sequence #status predicted <PFH>1-1-17/Domain: signal sequence #status predicted <PFH>1-1-17/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>1-1-17/Domain: leu
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Best Local S
Matches 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;146-169/Domain:
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                                                                      n: transmembrane #status predicted <TM1>
n: transmembrane #status predicted <TM2>
n: transmembrane #status predicted <TM2>
n: transmembrane #status predicted <TM3>
n: transmembrane #status predicted <TM4>
n: transmembrane #status predicted <TM5>
n: transmembrane #status predicted <TM6>
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n: transmembrane #status predicted <TM7>
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leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
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22.7%;
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Pred. No. 0.06
41; Mismatches
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for residue 488 as Arg
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/ protein
/ protein
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(covalent) #status predicted
protein kinase C) #status pre
protein kinase C) #status pre
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Matches 8	hes 84; Conservative 75; Mismatches 151; Indels 183; Gaps	16;
QY		121
Db	98 HEIRIEKANNL-LYINPEAFONLPNLRYLLISNTGIKHLPDVHKIHSFOKVLLDIODNIN	156
ξŞ	122 INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL	181
DЬ	157 IHTIERNSFVGLSPESVILWLNKNGIQEIHNCA	189
Ş	182 ARQLNPIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR	241
Db	190FNGTQLDELNLSDNNNLEBLPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKLRA 246	246
Ş	242 NQQSDPYKIPIBIVNKTLPIVAITLLSLVY	271
ᇝ	247 RSTYNIKKIPSLEKIVALMEASITYPSHCCAFANWRRQISELHPICNKSILRQEV	301
Ş	272LAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLG	306
Дb	302 DYMTQTRGQRSSLAEDNESSYSRGFDMTYAEFDYDLCNEVVDVTCSPKPDAFNPCEDILG	361
Qy	IENS	348
Dβ	362 YNILRVLIWEISILAITGNIIVLVTLTTSQYKLTVPRFLMCNLAFAD	408
γ		399
96	409LCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTVFASELS	456
Qy	400YVALLISTEHLLLYGWKRAFEEEZYYRFYTDPNFV-LAL	436
Db .	457 VYTLTAITLERWHTITHAMQLDCKVHVRHAASVMVMGWIFAFAAALFPIFGISSYMKVSI	516
\$	437 VLPSIVILDILQL 449	
D _P	517 CLPMDIDSPLSQL 529	

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protein YP8132.01

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A;Reference number: S52519

A;Accession: S52519

A;Accession: S52519

A;Accession: S52519

A;Coss-references: EMBL:248483; NID:g683777; PID:g683778; MIPS:YPL012w

A;Experimental source: strain AB972

C;Genetlos:
A;Genet SGD:RRP12

A;Cross-references: SGD:S0005933

A;Map position: 16L

C;Reywords: transmembrane #status predicted <TM1>
F;125-141/Domain: transmembrane #status predicted <TM2>
F;770-736/Domain: transmembrane #status predicted <TM3> RESULT 14

S59681

S59681

Sprobable membrane protein YPL012w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein LPA5w; hypothetical protein

C;Species: Saccharomyces cerevisiae

C;Date: 13-Jan-1996 #sequence_revision

C;Accession: S59681; S52519

C;Accession: S59681; Bussey, H.; Fortin, N.; Friesen, J.D. Storms

R;Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D. Storms A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI l A;Reference number: S59677 A;Accession: S59681 A;Molecule type: DNA A;Residues: 1-1228 cHAL> A;Residues: 1-1228 cHAL> A;Cross-references: EMBL:(33335; NID:g965076; PID:g965081; MIPS:YPL012W R;Badcock, K.; Churcher, C. Submitted to the EMBL Data Library, February 1995 R;Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N submitted to the EMBL Data Library, August 1: A;Description: The sequence of Saccharomyces 01-Mar-1996 #text_change 19-Apr-2002 N.; Friesen, 1995 J.D.; Storms, R.K.; Vo, XVI left arm Σ

Qy	Query M Best Lo Matches	C; Accession: R;Ng, W.V.; Leithauser Jung, K.H.; Proc., Natl. A;Authors: H. A;Authors: Gen A;Accession: A;Accession: C;Superfamili	RESULT 15 B84410 hypothetical C;Species: H C;Date: 02-F	Db	δ.	B 8	дь	γŞ	P 54	d d	ς <u>β</u>	ş 8	Db Cy	Db .	Qy	₽ \$, 5	P &	Query M Best Lo Matches
37 GSGDFAKSLTIRLIRCGYH-VVIGSRNPKFASEFFPHVVDVTHHEDAL 83	Match 4.7%; Score 110.5; DB 2; Length 222; Local Similarity 24.3%; Pred. No. 0.2; es 49; Conservative 34; Mismatches 94; Indels 25; Gaps 6;	Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hou ; Alam, M.; Freitas, T. Acad. Sci. U.S.A. 97, 12176-12181, 2000 Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A. nome sequence of Halobacterium species NRC-1. number: A64160; MUID:20504483; PMID:11016950 i: B84410 i: B84410 i-222 <stc> erences: GB:AE004437; NID:g10581987; PIDN:AAG2 22607C ly: conserved hypothetical protein MJ1501</stc>	15 tical protein Vng2607c [imported] - Halobacterium sp. NRC-1 es: Halobacterium sp. NRC-1 02-Feb-2001 #sequence revision 02-Feb-2001 #text change 16-Feb-2001	755 ALIQKRAYRIIT 766	LIYGWKRAFEEEYYRFYT 428	352 BEVWRLEMYISFGIMSLGLISLIAVISIPSVENALUREFSFIQSTLGYVALLISTFH 409	STNILAVLENVYTQTTPNARSYILETIDQYLKITSKEDLE	FFFAMVHVA	270 VYLAGLIAAAYQLYYGTKYRRFPPWLETWLQCRK 303	534 APYIKSFQKFDKVPDESIQLRVFQTIVDQIWSTLPRFCELPMDLRESFTDEFASELSSL 593	PGRAWLLELIRDYTKNANLATFQNEL	89PIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATEFFLYSFVRDVI	138 PDSLIVKGFNVVSAWALQLGPKDASRQYXICSNNIQARQQVIBLARQLNFI 188	网	84TKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPESNAEYLASLF 137	352 RKIPGVFHINCTYLASETPEVYQAASQCLISILSESVKDDLLLYTPSVDEKVPKNVD 408	STREET LISSGERABINGTER VEDITE KENAPTEN VOITELT NOW TAVALKERSET KEHOPEKAL	KSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLI :: : : : : : : : :	Match 4.7%; Score 111.5; DB 2; Length 1228; Local Similarity 19.9%; Pred. No. 1.5; es 111; Conservative 71; Mismatches 152; Indels 225; Gaps 28;

Search completed: March 2, 2004, 06:12:46 Job time : 51 secs

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1 MESISMMGSPKSLSETCLPN.....ALVLPSIVILDLLQLCRYPD
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Sequence 1, Application US/09083521 Patent No. 6048970 GENERAL INFORMATION:
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94 4.0 292 4 US-09 93 4.0 293 4 US-09 93 4.0 293 4 US-09 93 3.9 40.5 4 US-09 93 3.9 40.5 4 US-09 94 3.9 40.5 4 US-09 95 3.9 40.5 4 US-09 96 3.9 550 4 US-09 97 3.8 380 4 US-09 98 3.8 380 4 US-09 99 3.8 380 4 US-09 99 3.8 380 4 US-09 90 3.8 500 4 US-09	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	0
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	2, App	~	7, Appl	26, App	6381, A	7503, A	3105, A	6026, A	281, App	23822, A	Appli	5605, A	9411, A	7077, A	3, Appl	•	35, App	•

ALIGNMENTS

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APPLICANT: Rene S. Hubert

APPLICANT: Rene S. Hubert

APPLICANT: Kahan Leong

APPLICANT: AITHUR B. Raitano

APPLICANT: Douglas C. Saffran

APPLICANT: Douglas C. Saffran

APPLICANT: Douglas C. Saffran

APPLICANT: Steve Chappell Mitchell

TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO

FILLE REFERENCE: 129.16USU2

CURRENT APPLICATION NUMBER: US/09/323,873A

CURRENT FILING DATE: 199-06-01

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 32

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 173

TYPE: PRT

ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                         Query Match 38.3%; Score 901; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 1.4e-86;
Matches 173; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                246 DFYKIPISIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQL
                                    366 MSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRA 418
                                                                                                                                               306 GLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGI
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Best Local Similarity 100.0%; I
Matches 141; Conservative 0;
                                                                                                                                                                                                                                                          Sequence 2, Application US/09323873A Patent No. 6329503
                                                 APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERVENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
                                                                                                                                                                          APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO:
            CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: JEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: Herewith
CLASSIFICATION:
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ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
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APPLICATION NUMBER:
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T: Corley, Neil
INVENTION: PRO:
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APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

FITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REPERBNCE: 210121.427C21

CURRENT APPLICATION NUMBER: US/09/685,166A

CURRENT FILING DATE: 2000-10-10

NUMBER OF SEQ ID NOS: 898

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 879

LENGTH: 339

TYPE: PRT

CRGANTO:
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US-09-685-166A-879
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, TYPE: PRT
, ORGANISM: Homo Sapiens
US-09-323-873A-2
                                                                                                                     ; ORGANISM: Homo sapiens US-09-685-166A-879
                                                Query Match 30.5%; Score 717; DB 4; Best Local Similarity 54.9%; Pred. No. 8.5e-67; Matches 130; Conservative 48; Mismatches 59
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LENGTH: 3
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Best Local Similarity
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PRIOR PELICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
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208 LFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIBIVNKTLPIVAITLL
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Dillon, Davin C.
Mitcham, Jennifer L.
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Kalos, Michael
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lck, Thomas S
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Pred. No. 8.5e-67;
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                                                                                                                                                                                                                                                            RESULT 6
US-09-651-941-17
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US-09-655-270A-15
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TITLE OF INVENTION: High Density Sampling of
FILE REFERENCE: BC1011 US NA
CURRENT APPLICATION NUMBER: US/09/655,270A
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 1999-February-19
PRIOR APPLICATION NUMBER: 60/152,542
PRIOR APPLICATION NUMBER: 60/152,542
PRIOR FILING DATE: 1999-September-03
NUMBER OF SEQ ID NOS: 37
NUMBER OF SEQ ID NOS: 37
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LENGTH: 227
                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ROUVIER
APPLICANT: WALTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/09655270A Patent No. 6329151 GENERAL INFORMATION:
                                                                                                                                                                                                                    Sequence 17, Application US/09651941
Patent No. 6355470
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                                                     APPLICANT: ROUVIER, PIERRE E
APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITIE OF INVENTION: Genes Encoding Picric
FILE REFERENCE: BC1022 US NA
CURRENT APPLICATION UNMERR: US/09/651,941
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,545
PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 AADNASAAADCPIILLVVPYDGHRELVS---ELAPIFAGKLVVSCVNPLGFDKSGAYGLD
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Similarity 28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKSSKIAVVG--GTGPOGKGLAYRFAAAGWPVVIGSRSAERAEEAALEVRRRAGDGAVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsoft Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 6.4e-07;
                                                                                                                    Acid Degradation
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RESULT 8
US-08-487-886-2
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; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-955-597-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Rhodococcus erythropolis HL PM-1 US-09-651-941-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Mic; SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.0
Matches 60; Conservative
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SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Patent No. 6461856
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
FILE REFERENCE: BC1022 US NA
CURRENT APPLICATION NUMBER: US/09/955,597
CURRENT FILING DATE: 2001-09-17
CURRENT FILING DATE: 2001-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/152,545
PRIOR FILING DATE: 1999-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROUVIER,
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TYPE: PRT
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                                                                                                                                                           116 VEEGSAAEQLRDLVPGATVVAAFHHLSAVNLWEHE-GP--LPEDVLVCGDDRSAKDEVAR 172
                                                                              173
                                                                                                                    181 LARQUAFIP-IDLGSUSSAREIENLPLRUFTLWR 213
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                                                                                                                                                                                                 QYPESNAEYLASLFPDSLIVKGFNVVSA---WALQLGPKDASRQVYICSNNIQARQQVIE
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28.0%; Pred. No. 6.4e-07;
ative 33; Mismatches 88
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Pred. No. 6.4e-07;
3; Mismatches 88
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Sequence 2, Application US/08487886 Patent No. 5744448
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670,085
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOKET NUMBER: US/252
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: Kelton
APPLICANT: Schwei
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5" di
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APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 5744448een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
NUMBER OF SEQUENCES: 2
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LOCATION: 382 to 404
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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    NAME/KEY:
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IDENTIFICATION METHOD: similarity with other IDENTIFICATION METHOD: dimeric glycoprotein receipentification METHOD: domains, hydrophilic
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ADDRESSEE: Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
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putative transmembrane region III 427 to 448
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Best Local &
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LOCATION: 557 to 580
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD: similarity to other (IDENTIFICATION METHOD: protein-coupled recept DENTIFICATION METHOD: hydrophobic, about 20
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LOCATION: 512 to 533
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 HEIRIEKANNI-LYINPEAFQNLENLQYLLISNTGIKHLPDVHKIHSLQKVLLDIQDNIN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 HEDALTKTNIIFVAIHREHYTSLWDLRHLLVG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 4.6%; Score 107.5; DB 1;
Similarity 17.0%; Pred. No. 0.028;
84; Conservative 77; Mismatches 148;
ICLEMDIDSPLSQL 529
                               LVLPSIVILDILQL 449
                                                                                                                                                                                                                                              G----LLSFFFAMVHVA--
                                                                                                                                                                                                                                                                              VDYMTQTRGQRSSLAEDNESSYSRGFDMTYTEFDYDLCNEVVDVTCSPKPDAFNPCEDIM
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                                                                   SVYTLTAITLERWHTITHAMOLDCKVOLRHAASVMVMGWIFAFAAALFPIFGISSYMKVS
                                                                                                       G---YVALLISTEH------------VLIYGWKRAFEEEYYREYTPPNEV-LA 435
                                                                                                                                                                       SWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWRE-----FSFIQSTL
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COMDUTER: IBM P5/2,
COMDUTER: IBM P5/2,
OPERATING SYSTEM: MS-DOS version ...
OPERATING SYSTEM: MS-DOS version ...
OPERATING SYSTEM: MS-DOS version ...
SOFTWARE: VAX/VMS Massil via Kermit to
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,855
FILING DATE: 07-UN-1995
CLASSIFICATION DATA:
APPLICATION UMMBER: 07/670,085
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
NAME: Williams, Stephan P.
NAME: Williams, Stephan P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-08-482-855-2
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: 3.5" diskette, 1.44 MB, )

COMPUTER: IBM PS/2, model 55 SX

COMPUTER: IBM PS/2, model 50 SX

COMPUTER: MS-DOS version 4.0
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 723-1300
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APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 6121016een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                        NAME/KBY: putative transmembrane region I LOCATION: 350 to 370 IDENTIFICATION METHOD: similarity to other IDENTIFICATION METHOD: protein-coupled recommendation of the protein coupled r
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IDENTIFICATION METHOD: similarity with other IDENTIFICATION METHOD: dimeric glycoprotein reco
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TOPOLOGY: Linear
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ADDRESSEE: Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
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similarity to other G protein-coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length
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Matches 84;
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NAME/KEY: putative tran LOCATION: 427 to 448 IDENTIFICATION METHOD: IDENTIFICATION METHOD:
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LOCATION: 512 to 533
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RESULT 10
US-08-474-986-2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5" diskette, 1.44 MB, high COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0 SOFTWARE: VAX/VMS Massl1 via Kermit to IBI CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/474,986
FILING DATE: 07-Un-1995
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 723-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/670,085 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schweickhardt, Rene Lynn
Cheng, Shirley Vui Yen
Nugent, No. 637271leen Patrice
TITLE OF INVENTION: Human Follicle Stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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361
                                  306
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                                                                                                                                                                                                                 190
                                                                                                                                                                                                                                                    182 ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR 241
                                                                                                                                                                                                                                                                                        157
                                                                                                                                                                                                                                                                                                                         122 INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181
                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                79
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 GYNILRVĹIWFISILAITGNIIVLVILTTSQYKLTVP--
                                                                                                                                            RSTYNLKKLP-----TLEKLVALMEASLTYPSHCCAFANWRRQISELHPICNKSILRQE 300
                                                                                                                                                                             NQQSDFYKIPIEIVNKTL-PIVAITLLSLVY-----
                                                                                                                                                                                                                                                                                                                                                              HEIRIEKANNI-LYINPEAFQNLPNLQYLLISNTGIKHLPDVHKIHSLQKVLLDIQDNIN 156
                                                                                                                                                                                                                                                                                                                                                                                                HEDALTKINIIFVAIHREHYTSLWDLRHLLVG------
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ADDRESSEE: Stephan P. Williams,
Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
CITY: Boston
                                                                     VDYMTQTRGQRSSLAEDNESSYSRGFDMTYTEFDYDLCNEVVDVTCSPKPDAFNPCEDIM
                                                                                                                                                                                                                 ---FNGTQLDELNLSDNNNLEELPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKLRA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
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                                  ---LLSFFFAMVHVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kelton, Christie Ann
Schweickhardt, Rene 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6%; Score 107.5; DB 4;
17.0%; Pred. No. 0.028;
                                                                                                                                                                                                                                                                                        --TIERNŚFVGLSFESVILWL----NKNGIQEIHNCA--
                                                                                                       -LAGLLAAAYQLYYGTKYRRF-----
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                                  YSICLPMRRSERYLFILMMAYQQVHANIEN 347
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---RFLMCNLAFAD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 695;
                                                                                                       -----PPWLETWLOCKKOL 305
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                                                                       360
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GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEC
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND T
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8165
LENGTH: 940
TYPE: PRT
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US-09-323-873A-20
                                                                               ; ORGANISM: Acinetobacter baumannii US-09-328-352-8165
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-323-873A-20
                                                                                                                                                                                                                                                                                                                                                                            US-09-328-352-8165
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SEQ ID NO 20
LENGTH: 34
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                    Sequence 8165, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09323873A Patent No. 6329503
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Best Local
                  Query Match
Best Local S
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  Matches
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APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 129.16USUZ
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
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APPLICANT: Rene S. Huber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: STEAP-1 PEPTIDE
                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 SWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWRE------
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20; Conserv
    71; Conservative
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ilarity 58.8%;
Conservative
4.4%; Score 102.5; D. 19.5%; Pred. No. 0.15; tive 74; Mismatches
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Pred. No. 0.0003;
5; Mismatches
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                                       DB 4;
    146;
                                                                                                                                                                                                                                                           ID SEQUENCES RELATING TO ACINETOBACTER AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 34;
      Indels
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                                         Length 940;
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    73;
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US-09-316-083-3
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Best Local s
Matches 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09316083A Patent No. 6280942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: The Institute of Physical and Chemical Research TITLE OF INVENTION: Endonuclease FILE REFERENCE: PH-651
CURRENT APPLICATION NUMBER: US/09/316,083A
CURRENT FILING DATE: 1999-05-20
EARLIER APPLICATION NUMBER: JP98/141861
EARLIER FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 476
                                                                401
                                                                                                                               348
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452
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                                                                                                                                                                                                                               104 LRHLLVGKILIDVSNNMRINQYPESNAEYLASLF--PDSLIVKGFNVVSAWALQLGPKDA 161
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                                                                                                                                                                                                                                                                                                                                                      Similarity
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DNYDYYYYNKY
                            AAYQLYYGTKY
                                                                                                                                                                                                INNKLPIKNIMDIKNNYWLAGFTAADGSFLSSMYNPKDTLLFKNM----------
                                                                                                                                                                                                                                                                     NPYFVNAFSINI --
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                                                                                             LATFFFLYSFVRDVIHPYARNQQSDFYKIP----IEIVNKTLPIVAITLLSLVYLAGLLA 277
                                                                                                                              -RPSYVIS-QVETRKELIYLIQE----SFDL-SISNVKKVGNRKLKDFKLFTRTTDELMK 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVFLTLVFSHHFGV--ITSLTTASILFTILLAITVFLSLKQQAIYLAILALGMAYAAPLV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLSVLAKSFFILAVAFFALIFPLAKGAHWTAIGWVAQGTALIV---WGVTERYRLSRYI- 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLGLLSFFFAMVHVA-YSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYIS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAREIENLPLRLFTL-WRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIV 255
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                                                                                                                                                                                                                                                                                                                                                      4.3%;
                            288
462
                                                               DKFLPLHDNKQFNYIKFRFNTFİKSYNWNNRVFGLVLSE--YINNIKI
                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 3
Pred. No. 0.075;
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                   -KTNLAKEKIFTNIYNKLYSDYKINQINNHIPYYNYLK 302
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                                                                                                                                                                                                                                                                                                                                                                      DB 3;
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                                                                                                                                                                                                                                                                                                                                                                  Length 476;
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LENGTH: 476;
TYPE: PRT;
ORGANISM: Saccharomyces cerevisiae
US-09-933-700-3
                                              US-09-252-991A-21494
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US-09-933-700-3
                                                                                                 PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21494
LENGTH: 724
                                                                                                                                                                                                                                                                                                 Sequence 21494, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09933700 Patent No. 6528296 GENERAL INFORMATION:
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TITLE OF INVENTION:
FILE REFERENCE: 107
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NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 09/316,083
PRIOR FILING DATE: 1999-05-20
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                                                     TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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Query Match 4.3%; Score 101; DB 4; I Best Local Similarity 20.5%; Pred. No. 0.14; Matches 72; Conservative 57; Mismatches 105;

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P42945 saccharomyc	P38781 saccharomyc		P46896 gallus gall	Q10934 caenorhabdi	P03910 bos taurus			Q9jmh8 mus musculu		047423 branchiosto	Q8bfq3 mus musculu

ALIGNMENTS

RESULT 1 STEA_HUMAN SEQUENCE FROM N.A. MEDLINE=20056277, PubMed=10588738; Hubert R.S., Vivanco I., Chen B., Rastegar S., Leong K., Mitchell S.C., Madraswala R., Zhou Y., Kuo J., Raitano A.B., Jakobovits A., Saffran D.C., Afar D.E.H.; "STEAP: a prostate-specific cell-surface antigen highly expressed human prostate tumors"; human prostate tumors "; Proc. Natl. Acad. Sci. U.S.A. 96:14523-14528(1999). SEQUENCE FROM N.A. SEQUENCE FROM N.A. Abu-Threideh J., Stoneking T., Langston Y., Maupin R.; Chhmitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. Homo sapiens (Human). Eukaryota; Metazoa; (Mammalia; Eutheria; E Q9UHE8; 095034; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its Six transmembrane epithelial antigen of prostate STEAP OR STEAP1. STEA_HUMAN SEQUENCE FROM N.A. NCBI_TaxID=9606; STANDARD; Chordata; Primates; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. PRT; ₿ ij

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                                                SEQUENCE FROM N.A.

STRALN=JAL-1 / DSM 2661 / ATCC 43067;

STRALN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Googyne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

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Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
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01-NOV-1997
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                                           "Complete genome jannaschii.";
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                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative F420-dependent NADP
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GO:0005887; C:integral to plasma membrane; TAS.
GO:000591; C:intercellular junction; TAS.
GO:0015267; F:channel/pore class transporter ac
ince 273:1058-1073(1996).
FUNCTION: Catalyzes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF186249; AAF17479.1; -.
AC005053; AAC795150.1; ALT INIT.
AC004969; AAD15620.2; -.
BC011802; AAH11802.1; -.
V; HGNC:11378; STEAP.
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(Rel. 35, Last sequence update)
(Rel. 42, Last annotation updat
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F4RE_METTH
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Best Loc
Matches
STRAIN-Delta H;

MEDLINE=98037514; PubMed=9371463;

Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Aldredge T., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).
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Pfam; PF03807; F420_oxidored; 1.
TIGRPAMS; TIGR000301; TIGR00301; 1.
Hypothetical protein; Oxidoreductase; NADP;
SEQUENCE 223 AA; 24068 MW; 2370BBD6F5BBI
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                                                                                                                                                                                                               Archaea; Euryarchaeota;
Methanobacteriaceae; Me
                                                                                                                                                                                                                                        Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                          MTH248
                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
Putative F420-dependent NADP reductase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; MJ1501;
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                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                              NCBI_TaxID=187420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reduction of NADP(+) with F420H(2). dependent oxidation of the alcohol t dependent reduction of CO(2) to meth similarity).

CATALYTIC ACTIVITY: NADPH + coenzyme
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SIMILARITY:
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Methanothermobacter
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Best Local S
Matches 49
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Mammalia; Eutheria; F
Cercopithecinae; Maca
NCBI TaxID=9541;
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Follicle sti
        MEDLINE=94071854; PubMed=7504463;
Gromoll J., Dankbar B., Sharma R.S., Nieschlag E.;
"Molecular cloning of the testicular follicle stimulating receptor of the non human primate Macaca fascicularis and identification of multiple transcripts in the testic.";
Biochem. Biophys. Res. Commun. 196:1066-1072(1993).

-I- FUNCTION: Receptor for follicle stimulating hormone. To this receptor is mediated by G proteins which active the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stimulation of the stim
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P32212;
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                                                                                                                                                                                                                                                                                                                                   Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                         receptor)
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PIR; A69131; A69131.
InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420 oxidored; I.
TIGREPAMS; TIGR00301; TIGR00301; 1.
Hypothetical protein; Oxidoreductase; NADP; Complete p: SEQUENCE 232 AA; 24539 MW; ALCESOAHC8474296 CRC64;
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SIMILARITY: TO
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993 (Rel. 27, Last sequence update)
903 (Rel. 41, Last annotation update)
stimulating hormone receptor precursor
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cyclase
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Chordata;
                                                                                                                                                                                                                                                                                         Primates; Catarrhini;
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23.8%;
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(+) with F420H(2). Probably couples the NAI
on of the alcohol to the aldehyde with the
on of CO(2) to methane (anabolic function)
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Pred. No. 0.02
12; Mismatches
                                                                                                                                                                                                                                                                                                           ng macaque) (Cynomolgus monkey).
Craniata; Vertebrata; Euteleostomi;
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Pfam; PF01462; GPCRHODOPSN.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Transmembrane;
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SIMILARITY: Belongs to family 1 of G-protein coupl
FSH/LSH/TSH subfamily.
SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-i- SUBCELLULAR LOCATION: Integral membrane protein -i- SIMILARITY: Belongs to the UPF0191 family.
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Pasteurellaceae; Pasteurel
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HSSP; P23945;
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F79763; Q90719;
01-NOV-1997 (Rel. 35, Created)
01-NOV-997 (Rel. 35, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Follicle stimulating hormone receptor
                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a cotween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                       adenylate cyclase.
-i- SUBCELLULAR LOCATION: Integral membrane
-i- SIMILARITY: Belongs to family 1 of G-pro
FSH/LSH/TSH subfamily.
-i- SIMILARITY: Contains 7 leucine-rich (LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97473503; PubMed=9332357; Wakabayashi N., Suzuki A., Hoshino H., Nishimori K., Miz Wakabayashi N., Suzuki A., Hoshino H., Nishimori K., Miz "The cDNA cloning and transient expression of a chicken a follicle-stimulating hormone receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
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SMART; SM00013; LRRNT; 1.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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CYTOPLASMIC (POTENTIAL)
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Pred. No. 0.87;
2; Mismatches 173;
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FOLLICLE STIMULATING HORMONE EXTRACELLULAR (POTENTIAL).

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R PIR; S50969; S50969.

R GermOnline; 142046; -.

SGD; S0003974; FRE6.

DR InterPro; IPR002916; Ferric_reduct.

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X3 Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
X4 Johnston M., Hillier L., Riles L., Dubois E., Duesterhoeft A.,
X5 Benes V., Brueckher M., Delius H., Dubois E., Duesterhoeft A.,
X6 Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
X7 Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
X8 Louis E.J., Nessenguy F., Mewes H.-W., Miosga T., Moestl D.,
X9 Andeller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
X9 Andeller-Auer S., Nentwich U., Obermaier B., Rieger M., Rinke M., Rose M.,
X9 Andeller B., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
X9 Andeller M., Scherens B., Scholler P., Schwager C., Schwarz S.,
X9 Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
X9 Vierendeels F., Voet M., Volckaert G., Voss H., Manbutt R., Wedler E.,
X9 Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
X1 "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
X1 Nature 387:87-90(1997).
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15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ferric reductase transmembrane component 6 precursor (EC 1.16.1.
(Ferric-chelate reductase 6).
FRE6 OR YLL051C OR L0593.
Saccharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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NP_BIND
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-i- CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + 2 Fe(2+)
-i- COFACTOR: FAD (Probable).

-i- SUBCELLULAR LOCATION: Integral membrane protein (Potent
-i- SIMILARITY: Belongs to the FRE / CYBB family.
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     SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
MEDLINE=96132030; PubMed=8553699;
MEDLINE=96132030; PubMed=8553699;
Casamayor A., Aldea M., Casas C., Herrero E., Gamo F.J.,
Lafuente M.J., Gancedo C., Arino J.;
"DNA sequence analysis of a 13 kbp fragment of the left arm
"DNA sequence analysis of a 13 kbp fragment of the left arm
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"DNA sequence analysis of a 13 kbp fragment of the left arm
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                                                                                                                  Saccharomyces cerevisiae (Baker's yeast
Eukaryota; Fungi; Ascomycota; Saccharor
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                        chelate reductase FRE7 OR YOL152W.
                                                                                                        NCBI_TaxID=4932
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18.8%;
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smembrane component 7 (E
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                                                                                                                               (Baker's yeast).
sota; Saccharomycotina; Saccharomycetes;
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                                                 PSHR HUMAN STANDARD; PRT; 695 AA
P23945; Q16225;
01-MAR-1992 (Rel. 21, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
Pollicle stimulating hormone receptor precu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z48239; CAA88276.1;
EMBL; Z74894; CAA99174.1;
PIR; S60385; S60385.
                               receptor) FSHR.
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Pfam; PF01794; Ferric_reduct; 1.
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Oxidoreductase; Electron transport;
Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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SUBCELLULAR LOCATION: Integ
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Primates;
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Pred. No. 1;
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VARIANTS ALA-307; MEDLINE=99318093; Cargill M., Altshu Shaw N., Lane C.R.
                                                ERRATUM. Cargill M., Al.
Shaw N., Lane |
Friedland L., |
Lander E.S.;
Nat. Genet. 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic
J. Mol.
[7]
                                                                                                                                                                                                                                                                                                                                       MEDLINE=96363672; PubMed=8747461;
Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier J
Hendrickson W.A., el Tayar N.;
"Structural predictions for the ligand-binding region
hormone receptors and the nature of hormone-receptor
Structure 3:1341-1353(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gromoll J., Ried T., Holtgreve-Grez H., "Localization of the human FSH receptor genomic probe comprising exon 10."; J. Mol. Endocrinol. 12:265-271(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gromoll J., Dankbar B., Gudermann T.;
"Characterization of the 5' flanking region
stimulating hormone receptor gene.";
Mol. Cell. Endocrinol. 102:93-102(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minegish
"Cloning
 VARIANTS ALA-307
MEDLINE=22054685;
                                                                                                                                                                                                                                                                                                                                                                                                      JI-37
3D-STRUCTURE MODELING OF 49-228.
MEDLINE=96363672; PubMed=8747461;
Jiang X., Dreano M., Buckler D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 286-695 FROM N.A., AND VARIANT MEDLINE=95000244; PubMed=7916967;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol.
                                                                                                                                                                                       of human
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Biochem. Biophys. Res. Commun. 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93075197; PubMed=1359889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The cloning of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93246012; PubMed=1301382; Kelton C.A., Cheng S.V., Nugent N.P Rosenthal J.L., Overton S.A., Wands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem.
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                                                                                                                                                                   man genes.";
Genet. 22:231-238(1999)
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and sequencing of human FSH receptor cDNA.
Biophys. Res. Commun. 175:1125-1130(1991).
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18093; PubMed-10391209;
Altshuler D., Ireland J., Sklar P.,
ne C.R., Lim E.P., Kalyanaraman N., I
n, Rolfe A., Warrington J., Lipshutz
                                                                               Altshuler D., Ireland J., Sklar
ne C.R., Lim E.P., Kalyanaraman
., Rolfe A., Warrington J., Lips
                                                    23:373-373 (1999)
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AND SER-680.
; PubMed=12059813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             he human follicle stimulating COS-7, CHO, and Y-1 cells."; inol. 89:141-151(1992).
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runcated isoform
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G.D., Kuzeja J.
                                                                                 Sklar P., Ardlie K., raman N., Nemesh J., 2, Lipshutz R., Daley G
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C:integral to membrane; TAS.
C:plasma membrane; TAS.
P:follicle stimulating hormone r
P:female gamete generation; TAS.
P:female gonad development; TAS.
P:G-protein coupled receptor pro

receptor

activity;

TAS

protein

signalin.

TAS

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EMBL; M65085; AAA52477.1; -
EMBL; M59900; AAB26480.1; -
EMBL; M59489; AAA52478.1; -
EMBL; X68044; CAA48179.1; -
EMBL; X73199; AAB32275.1; -
EMBL; S73526; AAB32225.1; -
EMBL; S73526; AAB3227.1; -
EMBL; M5761; CRHUFT

PDB; 1XUN; 15-MAY-97.

Genew; HGNC:3969; FSHR.
MIN; 136435; -
MIN; 136435; -
GO; GO:00016021; C:integral
GO; GO:0005886; C:plasma me
GO; GO:0007896; F:follicle
GO; GO:0007929; P:female ga
GO; GO:0008585; P:female ga
GO; GO:0008586; P:follicle
GO; GO:0008586; P:follicle
GO; GO:0008586; P:follicle
GO; GO:0008586; P:follicle
GO; GO:0008586; P:follicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOId=P23945-2; Sequence=VSP 001953, VSP 001954;
-!- TISSUE SPECIFICITY: Sertoli cells and ovarian granulosa cells.
-!- DISBASE: Defects in FSHR are a cause of ovarian hyperstimulation syndrome (OHSS) [MIM:608115]. OHSS is a disorder which occurs either spontaneously or most often as an iatrogenic complication of ovarian stimulation treatments for in vitro fertilization. The clinical manifestations vary from abdominal distention and discomfort to potentially life-threatening, massive ovarian enlargement and capillary leak with fluid sequestration. Pathologic features of this syndrome include the presence of multiple serous and hemorrhagic follicular cysts lined by luteinized cells, a condition called hyperreactio luteinalis.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-!- SIMILARITY: Contains 5 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a copyrent the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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New Engl. J.
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Simoni M.
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MEDLINE=22812037; PubN
Smits G., Olatunbosun
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Poncheville L., Chaplot S., Savagner
nlou N., Descamps P., Misrahi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenylate cyclase.
SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
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InterPro; IPR000372; LR
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sepontein coupled receptor; Transmembrane; Alternative Phosphorylation; Repeat; Leucine-rich repeat; Alternative
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IPR000372; LRR_Nterm
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3 (POTENTIAL)
CYTOPLASMIC (POTENTIAL)
4 (POTENTIAL)
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
5 (POTENTIAL)
CYTOPLASMIC (POTENTIAL)
6 (POTENTIAL)
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FOLLICLE STIMULATING HORMONE RIEXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC
LRR 1.
LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 5.
SY SIMILARIT
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Pred. No. 1.1
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Missing (in isofo
/FTId=VSP_001953
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7 (POTENTIAL).
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(GLCNAC...)
(GLCNAC...)
(in isoform
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RESULT 10
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                                                                                                                     EMBL; L31966; AAAB6933.1; -.
EMBL; AF025377; AAC24981.1; -.
HSSP, P23945; XXIN.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR Nterm.
Ffam; PF00001; 7tm_1; 1.
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01-FEB-1996 (Rel
15-DEC-1998 (Rel
28-FEB-2003 (Rel
Follicle stimula
             Pfam; PF00001; 7tm_1; 1.

Pfam; PF00560; LRR; 4.

Pfam; PF01462; LRRYT; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PMART; SM00013; LARNT; 1.

PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.

PROSITE; PS00237; G PROTEIN RECEP F1_2; 1.

G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL. the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foe entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Ovary;

Wang Y.F., Meyer K.B., Schmidt K., Wan S.J., Degen S.J.F.

la Barbera A.R.;

"Porcine follicle-stimulating hormone receptor.";

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                    adenylate cyclase.
-!- SUBCELULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupl
FSH/LSH/TSH subfamily.
-!- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96011644; PubMed=7590277;
Remy J.J., Lahbib-Mansais Y., Yerle M.,
Pajot E., Grebert D., Salesse R.;
"The porcine follitropin receptor: cDNA
expression and chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               mitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Receptor for follicle stimulating hormone. The
of this receptor is mediated by G proteins which activate
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998 (Rel. 37, Last sequence update)
9003 (Rel. 41, Last annotation update)
stimulating hormone receptor precursor
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rane; Glycoprotein; Signal; repeat.
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Pred. No. 1.9;
91; Mismatches
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FOLLICLE STIMULATING HORMONE RECEPTOR.
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CYTOPLASMIC (POTENTIAL).
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P58529;
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STRAIN-0157:H7 / RIMD 0509952;

MEDLINE-21156231, PubMed=11258796;

MEDLINE-21156231, PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T. Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

1- FUNCTION: Involved in the efflux of sugars. The physiological content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the cont
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MEDLINE=21074935; PubMed=11266551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
Nature 409:529-533(2001).
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature
[2]
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                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to major facilitator (TC 2.A.1.2) family.
                                                                                                                                                                                                                                                                                                                                                                                                        arabinose regulon (By SUBCELLULAR LOCATION: (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                          may be the reduction of the intracellular concentration sugars or sugar metabolites. Transports L-arabinose and lesser extent IPTG. Seems to contribute to the control c arabinose regulon (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Inner metabolical services of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
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RESULT 12
SOTB ECOLI STANDARD; PRT; 396
ID SOTB ECOLI STANDARD; PRT; 396
AC P31172; P76883; P77353;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence upda
DT 15-MAR-2004 (Rel. 43, Last annotation up
B Sugar efflux transporter.
GN SOTB OR B1528.
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EMBL; AP002557; BAB35558.
PIR; G90895; G90895.
PIR; H85721; H85721.
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EMBL;
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Carole S., Pichoff S., Bouche J.-P.,
"Escherichia coli gene ydeA encodes a major facilitator pump which
exports L-arabinose and isopropyl-beta-D-thiogalactopyranoside.";
J. Bacteriol. 181:5123-5125(1999).
-I- FUNCTION: Involved in the efflux of sugars. The physiological r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97251357; PubMed=9097039;
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Kashimoto K., Kimura S., Kitakawa M., Kotomura
Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
Motomura
Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.
DNA Res. 3:363-377(1996).
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[2]
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Transcriptional activation of ydeA, which encodes a member of major facilitator superfamily, interferes with arabinose accumend induction of the Bacherichia coli arabinose PBAD promoter. J. Bacteriol. 181:2185-2191(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93186717; PubMed=8383113;
Cohen S.P., Haechler H., Levy S.B.;
"Genetic and functional analysis of the
resistance (max) locus in Escherichia
J. Bacteriol. 175:1484-1492(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 217-396 FROM N.A. MEDLINE=93186717; PubMed=8383113;
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Riley M., Collado-Vides
Gregor J., Davis N.W., F
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STRAIN=K12 / MG16
MEDLINE=97426617;
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NCBI_TaxID=562;
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                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restrong non-profit institutions as long as its content ified and this statement is not removed. Usage by and ities requires a license agreement (See http://www.isb-send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           sugars or sugar metabolites.
lesser extent IPTG. Seems to
arabinose regulon.
SUBCELLULAR LOCATION: Integra
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nce 277:1453-1474(1997).
AE000250; AAC74601.1;
D90795; BAA15210.1; -.
D90796; BAA15218.1; -.
D90797; BAA15230.1; -.
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s J., Glasner J.D., Rode C.K., Mayhew G.F.,
Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Renal sodium-dependent phosphate transport protein 1 (Sodium/phosphate cotransporter 1) (Na(+)/PI cotransporter 1) (Renal sodium-phosphate transport protein 1) (Renal Na(+)-dependent phosphate cotransporter
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InterPro; IPR0079114; MFS.
InterPro; IPR007928; Sub_transporter.
Pfam; PF00083; Sugar tr; 1.
PROSITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EcoGene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M96235;
PIR; C64907; C
                                                                                                                           365
                                                                                                                                            398
                                                                                                                                                                                357
                                                                                                                                                                                                                                                                        184
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                                                                                                                                                                                                                                                                                                                                                             91
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 ဝ္တ
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                              VTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNFKFASEFFFHVVDVTHHEDALTKTNIIF
                                                                                                                          IGYVG-AVPAFAALIWSIIIFRRWPVTLEEQ
                                                                                                                                           LGYVALLISTEHVLIYG-----
                                                                                                                                                                                                                                    VQNIAGFSANF-----
                                                                                                                                                                                                                                                   ARN----QQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLE
                                                                                                                                                                                                                                                                      LIKLLPLLPSEHSGSLKSLPL---
                                                                                                                                                                                                                                                                                                        SLAIRMAPAGKRAQALSLIATGTALAMVLGLPLGRIVGQYFGWRMTFFAIGIGALITLLC
                                                                                                                                                                                                                                                                                                                        AWALQLGP--KDASRQVYICSNNIQARQQVIELAR-----QLNFIPIDLGSL-----
                                                                                                                                                                                                                                                                                                                                                            VAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EG11636; sotB.
                                                                                                                                                             IAMMIIGLGMQVKVLALAPDATDVAMALFSGIFNIGIGAGALVGNQVSLHWS-----MSM
                                                                                                                                                                             IEMY ISFGIMSLGLLSL-----LAVTSIPSVSN-----
                                                                                                                                                                                                -----ALVSTAIALLLVCLALLLPAANSE--
                                                                                                                                                                                                                TWLQCRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWR
                                                                                                                                                                                                                                                                                       -----SSAREIENLPLRLFTLWRGPVVVAISLAT-----FFFLYSFVRDVIHPY
                                                                                                                                                                                                                                                                                                                                           IASHVLSFLS-WSFTVLVISRI-------GVAFAHAIF------WSITA
                                                                                                                                                                                                                                                                                                                                                                               VPVGLL--SDIAQSFHMQTAQVGIMLTİYAWVVALMSLPFMLMTSQVERRKLİJCLFVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteome.
 NPTI
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81
103
136
170
275
275
299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C64907
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                               STANDARD;
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70
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                                                                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 104; DB
Pred. No. 1;
72; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                 146;
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Matches 76
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C TISSUB-Kidney;

K MEDLINE-95335846; PubMed=7611445;

K Chong S.S., Kozak C.A., Liu L., Kristjansson K., Dunn S.T.,

A Chong S.S., Kozak C.A., Liu L., Kristjansson K., Dunn S.T.,

A Bourdeau J.E., Hughes M.R.;

"Cloning, genetic mapping, and expression analysis of a mouse renaingular contains of the mouse renaingular contains of the sodium-dependent phosphate cotransporter.";

L Am. J. Physiol. 268:F1038-F1045(1995).

C -!- PUNCTION: Important for the resorption of phosphate by the kidure of the renaingular membrane.

C -!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUB SPECIFICITY: Kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
SEQUENCE
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MGD; MGI:103209; Slc17al.
InterPro; IPR007114; MFS.
InterPro; IPR004745; Pi cotranspt.
TIGREAMS; TIGR00894; 2A0114euk; 1.
PROSITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-siborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the sodium/phosphate cotransporter family.
                   269
                                                                                                                               188
                                                                                                                                                                                                                                                                                                                   110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X77241;
                                                                                                                                                                                                                                                                                                                                                      76;
                                                                                                                                                                                                                                                                                                                                                                        Similarity
--LVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMR
                                                                          GFICDLLGWPMVFYIFGIVGCVLSLSWFFLFFDDPKD--HPYMSSSEKDYIISSLMQQAS
                                                                                                                                                                                                   VCRVLQGIAQGTVSTGQHBIWVKWAPPLERGRLTS-----MTLSGFVM--GPFIVLLVS
                                                                                                                                                                                                                                         ICSNNIQARQQVIELARQLNFI----PIDLGSLSSAREIENLFLRLFTLWRGPVVV----
                                                                                                                                                                                                                                                                                                               GKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDA---SRQVY
                                                    SGRQSLPIKAMLKSLPLWAIILNSFAFIWSNSLLVTYTPTF1STVLHVNVRENGLLSSLP
                                                                                                                                                                                                                                                                              GLILSSVFFGMVVVQAP----VGYLSGIYPMKRIIGSSLFLSSLMSLLIPPAAQVGAALVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Symport;
79
117
1176
199
260
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2304
337
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAA54459.1;
                                                                                                                                                                                                                                                                                                                                                                                                                         , sodium
99
137
196
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280
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383
3419
449
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456
56
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                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transport; T
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                    Score 103; DB
Pred. No. 1.5;
64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.

N-LINKED (GLCNAC. . .

N-LINKED (GLCNAC. . .

N-LINKED (GLCNAC. . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                    142;
                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                      Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                    Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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InterPro; IPR001135; Oxidored 49kDa.
Pfam; PF00346; complex1 49Kd; 1.
PROSITE; PS00535; COMPLEX1 49K; 1.
Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast.
SEQUENCE 391 AA; 44913 MW; 9A40AEC68995B25E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend.an email to license@isb-sib.ch).
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
NAD(P)H-quinone oxidoreductase chain H, chloroplast (
NAD(P)H dehydrogenase, chain H) (NADH-plastoquinone
49 kDa subunit):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99398694; PubMed=10468594; Turmel M., Otis C., Lemieux C.; "The complete chloroplast DNA sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       olivacea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Chlorodendrales; Chlorodendraceae; Nephroselmis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=31312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nephroselmis olivacea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9TKV6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plastoquino1.
SIMILARITY: Belongs to the complex I 49 kDa subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE PLASTOQUINONE. COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE ENZYME
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                                                                                                                                                                                                                                         , OB
                                                                                                                                                                                                                                                              Similarity
NFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQOS
                                                                                                      --SNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQL
                                                                                                                                                                                             KTNIIFVAIHREHYTSLWDLRHLLV---GKILID-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLLAYICGILAGQMSDFFLTRK-----IFSIVTVRKLFTTLGSFCPVIFIMCLLYLSYN 359
                                                                                                                                                  KTDPMIVSM-GPHHPSMHGVLRLIVTLDGENVLDCEPVVGYLHRGMEKIAENRTIVQYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lete chloroplast DNA sequence of the green alga Nephroselmis insights into the architecture of ancestral chloroplast
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                           4.4%;
17.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NSTLSFSYCGQLINALDIAPRYYGFLKAVTALIGMFGGLISSTLA 415
                                                                                                                                                                                                                                       70;
                                                                                                                                                                                                                                  Score 102.5; 1
Pred. No. 1.3;
70; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                       124;
                                                                                                                                                                                                                                    Indels 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 1.6.5.-)
e oxidoreductase
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                                                                                                                                                                                             -VSNNMRINGYPE 127
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                Pfam; PF05252; UPF0191; 1.

Hypothetical protein; Transmembrane; Cc TRANSMEM 20 39 POTENTIAL. TRANSMEM 85 104 POTENTIAL. TRANSMEM 124 146 POTENTIAL. TRANSMEM 124 146 POTENTIAL. TRANSMEM 153 175 POTENTIAL. TRANSMEM 159 198 POTENTIAL. TRANSMEM 179 198 POTENTIAL. TRANSMEM 179 198 POTENTIAL. TRANSMEM 179 198 POTENTIAL. TRANSMEM 179 198 POTENTIAL. TRANSMEM 179 198 POTENTIAL. TRANSMEM 179 198 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FDB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation updat Hypothetical protein BMEII0304.
                                                                                                                                                                                         EMBL; AE009669; AAL53546.1; PIR; AG3547; AG3547.
                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- SIMILARITY: Belongs to the UPF0191 family.
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	Search completed: March 2004 23.31.14	ល
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172	Db 121 RPFITIGMISLALLVPLALTSNNWSIRKLGRRWSSLHK-LVYIAIAGSAVHFL 172	o
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120	Db 80 LLRYRRALGLLAFYYALMHFTTYMVLDQGLNLSAIITDIVR- 120	ם
357	Qy 299 -LQCRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEBEVWRI 357	ю
79	Db 20 LWLLYTAGEVPAVWTEYLGATGQLGADPVKTFEHLLGLWALRFLILTLLVTPMRDLTGIT 79	U
298	Qy 267 LSLVYLAGLLAAAYQLYYGTKYRRPPPWLETW	Ю
7;	Matches 43; Conservative 25; Mismatches 51; Indels 62; Gaps	
	Query Match 4.3%; Score 102; DB 1; Length 220; Best Local Similarity 21.8%; Dred No. 0.70.	

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US-10-239-607-29
US-10-239-190-27-574
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US-10-39-21-0-14
US-10-198-02-520-1
US-10-198-02-521-6
US-10-198-951-6
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Sequence 11, Appl
Sequence 12, Appl
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Sequence 13, Appl
Sequence 36, Appl
Sequence 38, Appl
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ALIGNMENTS

RESULT 1

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US-09-888-257A-10

Sequence 10, Application US/09888257A

Publication No. US20030060612A1

GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
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APPLICANT: Mool, William I.
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CURRENT APPLICATION NUMBER: US/009/888,257A
CURRENT PILLING DATE: 1990-04-30
PRIOR APPLICATION NUMBER: US/00/63,540

PRIOR APPLICATION NUMBER: US/00/63,540

PRIOR APPLICATION NUMBER: US/00/63,540

PRIOR APPLICATION NUMBER: US/00/63,678

PRIOR APPLICATION NUMBER: US/00/99,792

PRIOR APPLICATION NUMBER: US/00/99,792

PRIOR APPLICATION NUMBER: US/00/99,792

PRIOR APPLICATION NUMBER: US/00/99,792

PRIOR APPLICATION NUMBER: PCT/US/99/20111

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PRIOR APPLICATION NUMBER: PCT/US/99/20111

PRIOR APPLICATION NUMBER: PCT/US/99/20111

PRIOR APPLICATION NUMBER: PCT/US/99/00/4342

PRIOR APPLICATION NUMBER: PCT/US/90/05841

PRIOR APPLICATION NUMBER: PCT/US/90/05841

PRIOR APPLICATION NUMBER: PCT/US/90/05841

PRIOR APPLICATION NUMBER: PCT/US/90/06439
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; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; SEQ ID NO 10
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-888-257A-10
GENERAL INFORMATION:

APPLICANT: Agensys, Inc.

APPLICANT: Archur B. Raitano

APPLICANT: Arthur B. Raitano

APPLICANT: Douglas Saffran

APPLICANT: Daniel E.H. Afar

APPLICANT: Steven Chappell Mitchell

APPLICANT: Mary Faris

ITILE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO

FILE REFERENCE: 51158-20016.02

CURRENT APPLICATION NUMBER: US/10/165,044

CURRENT FILING DATE: 1998-06-01

PRIOR APPLICATION DATE: 1998-06-01
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Publication No. US20030149531A1
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PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR PILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: PCT/US00/33040
PRIOR PILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 57
SOFTMARE: FastSEQ for Windows Version 4.0
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                        EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
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RESULT 3
US-10-239-607-29
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Publication No. US20030219761A1
GENERAL INFORMATION:
APPLICANT: Saatcioglu, Fahri
TITLE OF INVENTION: No. US20030219761A1el Prostate-Specific or TITLE OF INVENTION: Testis-Specific Nucleic Acid Molecules, Polypeptides, TITLE OF INVENTION: Disgnostic and Therapeutic Methods FILE REFERENCE: 50218/003002 CURRENT FILING DATE: 2002-09-24 PRIOR APPLICATION NUMBER: US/10/239,607 CURRENT FILING DATE: 2002-09-24 PRIOR FILING DATE: 2001-03-23 PRIOR FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: WS 60/191,929 PRIOR FILING DATE: 2000-03-24 NUMBER OF SEQ ID NOS: 73 PRIOR FILING DATE: 2000-03-24 NUMBER OF SEQ ID NOS: 73 SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Workload of Diagnosis of Cancer, Compositions and TITLE OF INVENTION. Methods of Screening for Modulators of Cancer CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/335,334
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-21
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US-10-295-027-574
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100.0%; Score 2351;
Best Local Similarity 100.0%; Pred. No. 8e
Matches 454; Conservative 0; Mismatches
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o. US20030232350A1
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Similarity 100.0%; Pred. No. 8e-222;
54; Conservative 0; Mismatches 0;
ESYYRFYTPENFVLALVLPSIVILDLLQLCRYPD
                    EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD
                                                               ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
                                                                                               CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMY
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RESULT 5

Sequence 2, Application US/10392190

Publication No. US20040005598A1

GENERAL INFORMATION:

APPLICANT: Devaux, Bridgitte

APPLICANT: Eberhard, David

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Hillan, Kenneth J.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wasaura, Daniel G.

APPLICANT: Yansura, Daniel G.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: PUMPCn COMPOSITIONS AND USES

FILE REFERENCE: P2994RIC1-US
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THEREOF

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Sequence 3155, Application US/10104047

| Sequence 3155, Application US/2004047
| Publication No. US20030236392A1
| GENERAL INFORMATION:
| APPLICANT: HELIX RESEARCH INSTITUTE
| TITLE OF INVENTION: No. US20030236392A1e1 full length cDN
| FILE REFERENCE: H1-A0105
| CURRENT APPLICATION NUMBER: US/10/104,047
| CURRENT FILING DATE: 2002-03-25
| PRIOR APPLICATION NUMBER:
| PRIOR APPLICATION NUMBER:
| PRIOR FILING DATE:
| NUMBER OF SEQ ID NOS: 4096
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 3155
| LENGTH: 454
| TYPE: PRT
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US-10-104-047-3155
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; ORGANISM: Homo Sapien
US-10-392-190-2
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CURRENT FILING DATE: 2003-03-19
PRIOR APPLICATION NUMBER: US 60/235,451
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: PCT/US01/30290
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 14
SEQ ID NOS: 14
Query Match 99.9%;
Best Local Similarity 99.8%;
Matches 453; Conservative
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ilarity 100.0%;
Conservative 0,
Score 2348; DB 15;
Pred. No. 1.6e-221;
1; Mismatches 0;
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Pred. No. 8e-222;
; Mismatches 0
                                     DB 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09802520 Publication No. US20020187472A1 GENERAL INFORMATION:
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               LENGTH: 490
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
RAMEN: misc feature
NAMEN/KEY: misc feature
OTHER IMPORMATION: Incyte ID No. US20020187472A1 7492448CD1:-09-802-520-1
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: Chen, Huei-Mei
: Ison, Craig H.
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                                                                                                                                                                                                                        97.6%; Score 2294; DB 9; ilarity 100.0%; Pred. No. 3.5e-216; Conservative 0; Mismatches 0;
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RESULT 8
US-10-239-607-14
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TITLE OF INVENTION: No. US2030219761Alel Prostate-Specific or
TITLE OF INVENTION: Testis-Specific Nucleic Acid Molecules, Polypeptides,
TITLE OF INVENTION: Disgnostic and Therapeutic Methods
FILE REFERENCE: 50218/003002
CURRENT APPLICATION NUMBER: US/10/239,607
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/US01/09410
PRIOR APPLICATION NUMBER: PCT/US01/09410
PRIOR APPLICATION NUMBER: US 60/191,929
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 73
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/10239607
Publication No. US20030219761A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 443; Conserv
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nilarity 99.8%;
Conservative (
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Pred. No. 8.7e-216;
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TITLE OF INVENTION: No. US20030219761Alel Prostate-Specific or
TITLE OF INVENTION: Testis-Specific Nucleic Acid Molecules, Polypeptides, and
TITLE OF INVENTION: Diagnostic and Therapeutic Methods
FILE REFERENCE: 50218/003002
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US/10/239,607
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/US01/09410
PRIOR APPLICATION NUMBER: PCT/US01/09410
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-239-607-32
RESULT 10
US-10-182-951-6
US-10-182-951-6
Equence 6, Application US/10182951
Publication No. US20030138895A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
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US-10-239-607-32
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Publication No. US20030219761A1
GENERAL INFORMATION:
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Best Local Similarity 99.7%;
Matches 394; Conservative
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Pred. No. 5.7e-191;
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Indels Length

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TITLE OF INVENTION: DRUG METABOLIZING ENZYMES

FILE REFERENCE: PI-0033 PCT
CURRENT APPLICATION NUMBER: US/10/182,951
CURRENT FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: 60/181,856; 10/183,684; 60/185,141; 60/186,818; 60/188,345;
PRIOR RILING DATE: 2002-02-11; 2000-02-17; 2000-02-25; 2000-03-03; 2000-03-09; 2000-0
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PERL PROGram
SEQ ID NO 6
                                                                    Sequence 13, Application U Patent No. US20020146692A1 GENERAL INFORMATION:
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Best Local &
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APPLICANT:
APPLICANT:
                 APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
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NAME/KEY: misc_feature
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mes 242; Conser
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Tang, r. Tang, Chenghua
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AZIMZAI, Yalda
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YAO, Monique G.
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Leo L.
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54.5%; Pred. No. 6.4e-116;
tive 82; Mismatches 108;
                                                                                                        US/09747835A
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RESULT 12 US-10-239-607-36

Sequence 36, Application US/10239607 Publication No. US20030219761A1 GENERAL INFORMATION:

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APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
APPLICANT: Demanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIK
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT APPLICATION NUMBER: US/09/739
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/729,739
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
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PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
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PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
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TYPE: PRT
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Similarity 54.3%;
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                                      EEYYRFYTPPNFVLALVLPSIVIL 444
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                                                                             LSLGVLALGTLSLLAVTSLPSIANSLNWREFSFVQSSLGFVALVLSTLHTLTYGWTRAFE
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ESRYKFYLPPTFTLTLLVPCVVIL
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  444
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; APPLICANT: Saatcioglu, Fahri
; TITLE OF INVENTION: No. US20030219761A1el Prostate-Specific or
; TITLE OF INVENTION: Testis-Specific Nucleic Acid Molecules, Pol
; TITLE OF INVENTION: Diagnostic and Therapeutic Methods
; FILE REFERENCE: 50218/003002
; CURRENT APPLICATION NUMBER: US/10/239,607
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09410
; PRIOR APPLICATION NUMBER: PCT/US01/09410
; PRIOR APPLICATION NUMBER: DCS 60/191,929
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 73
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 73
                                                                                                                                                                                                                               RESULT 13
US-10-239-607-38
(S-quence 38, Application US/10239607; Publication No. US20030219761A1; GENERAL INFORMATION:
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US-10-239-607-36
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Best Local Similarity
Matches 241; Conserv
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SEQ ID NO 36
LENGTH: 488
                APPLICANT: Saatcioglu, Fahri
TITLE OF INVENTION: No. US20030219761A1el Prostate-Specific of TITLE OF INVENTION: Testis-Specific Nucleic Acid Molecules,
TITLE OF INVENTION: Diagnostic and Therapeutic Methods
FILE REFERENCE: 50218/003002
CURRENT APPLICATION NUMBER: US/10/239,607
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/US01/09410
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
      OF SEQ ID NOS: 73
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                                                                                                                                                                                                                                                                                            APPLICANT: LAL, Preeti
APPLICANT: YUE, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: AZIMZAI, Yalda
APPLICANT: BUGHN, Mariah R.
APPLICANT: LU, Dyung Aina M.
APPLICANT: DATTERSON, Chandra
                                                                                                                   CURRENT APPLICATION NUMBER: US/09/965,529
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
NUMBER OF SEQ ID NOS: 74
SOFTMARE: PERL Program
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Appublication No
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                                                                                                                                                                                                                                                        TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS FILE REFERENCE: PF-0731 USA
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte
                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                LENGTH: 459
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    No. US20020182671A1 1859305CDI
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 488
TYPE: PRT
                                                                                                                                                               361 ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE 420
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Pred. No. 1.3e-115;
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APPLICANT: LAL, Preeti; YUE, Henry
APPLICANT: TANG, Y. Ton; BANDMAN, Olga
APPLICANT: BAPGORD, Neil; AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
CUERENT APPLICATION NUMBER: US/09/969,680A
CUERENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/2315
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/164,203
PRIOR APPLICATION NUMBER: 60/164,203
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL PROGram
                                                                                   ) ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: misc_feature
, OTHER INFORMATION: Incyte ID No. US20030124649A1 1859305CD1
US-09-969-680A-21
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US-09-969-680A-21
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                                                                                                                                                                                                             SEQ ID NO 21
LENGTH: 459
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Best Local Similarity
Query Match
Best Local Similarity
Matches 204; Conserv
                                                                                                                                                                                                TYPE: PRT
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46.3%; Score 1088; DB 10; ilarity 46.9%; Pred. No. 6.6e-98; Conservative 89; Mismatches 136;
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46.9%; Pred. No. 6.6e-98;
ative 89; Mismatches 136;
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Search completed: March 2, 2004, 06:36:32 Job time: 66 secs 맑 Ś 밁 δ 밁 S В S 片 δ 밁 δ 밁 δ 밁 5

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Result
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Q99p41 rattus norv
Q8c159 mus musculu
Q80z13 mus musculu
Q80z147 mus musculu
Q80z15 homo sapien
Q7z389 homo sapien
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ALIGNMENTS

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B & B :	O	SOR	DR DR	2223	7	288888 8		RESULT Q8IUE7
	Query Match 97.4%; Score 2290; DB 4; Length 490; Best Local Similarity 99.8%; Pred. No. 4.1e-176; Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	THEFFTC; IFW04455; NADFOXTED F420. Pfam; PF03807; F420_oxidored; I. SEQUENCE 490 AA; 56027 MW; D1971A84880F7E51 CRC64;	Chem. 277:36689-36696 08445; AAG32149.1; 06118; P:electron trai	"Molecular f.; "Molecular cloning and characterization of STAMP1, a highly prostate specific six-trans-membrane protein that is overexpressed in prostate cancer.";	SEQUENCE FROM N.A. TISSUE=Prostate; MEDLINE=22229309; PubMed=12095985; Korkmaz K.S., Blb1 C.C., Korkmaz C.G., Loda M., Hager G.L.,	Homo sapiens (Human). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606;	01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-UN-2003 (TrEMBLrel. 24, Last annotation update) CTAMP1	LT 1 IB7 IB7 IB7 IB7 IB7 IB7 IB7 IB7 IB7 IB7

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Q8NFT2;
01-OCT-2002
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"Cloning and characterization of a novel six-transmembrane
STEAP2, down-regulated in androgen-independent prostate can
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF455138; AAN04080.1; -.
Genew; HGRC:17885; STEAP2.
Genew; HGRC:17885; STEAP2.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:006118; P:electron transport; IEA.
InterPro; IPR004455; NADPOXXEd F420.
Pfam; PF03807; F420_oxidored; I.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J; TISSUE-Head;
MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome k
60,770 full-length cDNAs";
Nature 420.563-573(2002).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Weakly similar to
4921538B17RIK.
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                                                                                                                                            LARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA
                                                                                                                                                                                                                                 RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE
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                                                                                                                                                                                                                                                                                                            RNPKFASBFFFHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM
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                                                                   RNQQSDFYKIPIBIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRPPPWLETWLQ
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CRKQLGLLSFFFAMVHVAYSLCLFMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMY
                                         RNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRPPPWLDTWLQ
                                                                                                                         LAROLNFIPVDLGSLSSAKEIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA
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(TIRMBLrel. 23, Last sequence up
(TIRMBLrel. 24, Last annotation
ar to tumor suppressor PHYDE.
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Rodentia;
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97.3%;
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Pred. No. 4.8e
9; Mismatches
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Best Local Similarity
Matches 248; Conser
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"Analysis of the mouse transcriptome based on
60,770 full-langth cDMAs.";
Nature 420:563-573 (2002).
EMBL; AK078769; BAC37383.1; -
EMBL; AK078769; BAC37383.1; -
MGD; MGI:1915679; Japps.
MGD; MGI:1915679; Japps.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPOXXED FEAD.
Pfam; PF03807; F420 oxidored; I.
SEQUENCE 488 AA; 54780 MW; FDFC4F42AE503DI
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Q8C5F0;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRALN=C57BL/60; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
DUDULIN 2 homolog.
TSAP6 OR 1010001D01RIK.
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Mammalia; Eutheria;
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                    GVLALGMLSLLAVTSLPSIANSLNWKEFSFVQSTLGFVALILSTMHTLTYGWTRAFEENH
                                              GIMSLGILSLLAVTSIPSVSNALNWREFSPIQSTLGYVALLISTFHVLIYGWKRAFEEEY
                                                                                                                   QIGLLSFFFAMLHALYSFCLPLRRSHRYDLVNLAVKQVLANKSRLWAEEEVWRMEIYLSL
                                                                                                                                             QLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISF
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Sciurognathi; Muridae;
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8.4e-98;
ches 100;
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Q99P41;
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ
EMBL; AF335281; AAX00361.1;
EMBL; AF335865; AAL78207.1;
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPoxxed F420.
Pfam; PF03807; F420_oxidored; I.
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Lu Y., Rinaldy A.R.,
Submitted (JAN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steiner M.S., Zhang X., Wang Y., Lu Y. "Growth inhibition of prostate cancer novel tumor suppressor gene, pHyde.";
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MEDLINE=20424188; PubMed=10969787;
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Mammalia; Eutheria; Rodentia;
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Nunning; TISSUE=Prostatic carcinoma;

Rinaldy A.R., Steiner M.S.;

Additional to the EMBL/GenBank/DD
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                                    GIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEY
                                                                                                                 QLGLLSFFFAMVHVAYSLCLPMRRSERYLFLMMAYQQVHANIENGWNEBEVWRIEMYISF
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Q80ZF3;
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01-JUN-2003
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01-MAR-2003 (TYEMBLYel. 23, Last sequence up
01-CCT-2003 (TYEMBLYel. 25, Last annotation
similar to RIKEN cDNA 1010001D01 gene.
TSAP6 OR 1010001D01RIK.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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MGD, MGI:1915678; Tapp6.
30, GO:0006118, P:electron transport,
InterPro, IPR004455, NADPoxred_P420.
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81; Mismatches
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Mus musculus (Mouse) Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

(Mouse)

Dudulin 2. TSAP6 OR 1010001D01RIK.

Last sequence update)
Last annotation update)

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ID 27
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Best Local S
Matches 248
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01-DEC-2001
01-DEC-2001
01-JUN-2003
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Roborel de Climens A., Fiucci G., Bouvard V., Tuynder M.,
Morchoisne S.P., Crible V., Lespagnol A., Dausset J., Oren
Amson R., Telerman A.;
"The p53-inducible TSAP6 gene product regulates apoptosis
cycle and interacts with Nix and the Mytl kinase.";
Proc. Natl. Acad. Sci. U.S.A. 100:2284-2289(2003).
EMBL, AY214462; AAO38239.1; -
GO: GO:0006118; P:electron transport; IEA.
InterPro; ITR004455; NADPOXTEE F420.
Pfam, PF03807; F420_oxidored; I.
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STRAIN-DSMZ ACC331; TISSUE=Bone ma
MEDLINE-22506415; PubMed=12606722;
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Mammalia; Eutheria; Rodentia;
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Best Local S
Matches 248
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"Molecular cloning and expression of mouse dudul;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ dat
EMBL; AY029586; AAK50539-1;

MGD; MGJ:1915678; Tsap6.

GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPoxred F420.

Pfam; PF03807; F420 oxidored; T.

SEQUENCE 514 AA; 57288 MW; 339886C288AEC0E2 (
                                                                                                                                                                                                                                       OB6SF6;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Similar to dudulin 2 (TSAP6).
SEQUENCE FROM N.A.

MEDLINE=22506415; PubMed=12606722;
Passer B.J., Nancy-Portebois V., Amzallag
Passer B.J., Nancy-Portebois O., Bouvard
                                                                                          Strausberg R.;
Submitted (JAN-2003)
                                                                                                                                                                                             Eukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Kidney;
                                                                                                                                                                         NCBI_TaxID=9606;
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81; Mismatches
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T "The p53-inducible TSAP6 gene product regulates apoptosis and
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I proc. Natl. Acad. Sci. U.S.A. 100:2284-2289(2003).

I EMBL; BC042150; AAH44150.l;
I EMBL; AV214461; AAO38238.l;
I EMBL; AV214461; AAO38238.l;
I ROG GO:0066118; P:electron transport; IEA.

NR GO; GO:0066118; P:electron transport; IEA.

NR GO; GO:0066118; P:electron transport; IEA.

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SQ SEQUENCE 488 AA; 54600 MM; C89EB0D0430F9BFB CRC64;
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SEQUENCE FROM N.A.
TISSUB-Human colon endothel primary cell of TISSUB-Human colon endothel primary cell of Secker H., Boecher M., Mewes H.W., Weil Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/I EMBL; B538047; CAD97986.1; -.
Hypothetical procein.
SEQUENCE 498 AA; 55593 MW; 69DD23D5A00
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Mammalia; Eutheria; Primates;
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Best Local S
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                                          EMBL; AK001691; BAA91839.1; --
EMBL; AK029585; AAK50538.1; --
GO; GO:0006118; P:electron transport;
InterPro; IPR003006; IG_MHC.
InterPro; IPR003006; NADPoxxed_F420.
Pfam; PF03807; F420_oxidored; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Statogai T., Ota T., Hayashi K., Sugano S., Aotsuka S., Yoshikawa Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yamamoto J., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;

"NEDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-UNN-2003 (TrEMBLrel. 24, Last annotation
Hypothetical protein FLJ10829 (Dudulin 2).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordara; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                       Serru V., Manivet P., Lenoir C., Eschwege P., Vaubourdolle M., Kellermann O., Loric S.; "Dudnlin 2, a new tumor antigen expressed in 'Submitted (APR-2001) to the EMBL/GenBank/DDBJ
Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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  188 AA;
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Pred. No. 4.4e-
82; Mismatches
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01-JUN-2003
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InterPro; IPR004455; NADPoxred
Pfam; PF03807; F420 oxidored; I
PROSITE; PS00290; IG MHC; 1.
SEQUENCE 487 AA; 54501 MW;
                                                                                                                                                              SEQUENCE FROM N.A.

Lu Y., Beheshti B., Squire J.A., Yang X.J.;

Lu Y., Beheshti B., Squire J.A., Yang X.J.;

"Characterization of a novel apoptosis inducing inhibits prostate cancer cell growth.";

submitted (MAR-2002) to the EMBL/GenBank/DDBJ EMBL; AY082873; AAM45136.1;

GO; GO:0006118; P:electron transport; IEA.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pred. No. 7.5e-
83; Mismatches
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Pred. No. 1.6e-92;
3; Mismatches 108;
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Best Local S
Matches 239
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"A novel prostate-derived tumor suppressor.";
submitted (FEB-2000) to the EMBL/GenBank/DDBJ da
EMBL; AF238864; AAL78206.1; -
GO; GO:0006118; P:electron transport; IEA.
InterPro; IFR003006; Ig MHC;
InterPro; IFR004455; NADPoxred F420.
Pfam; PF03807; F420 oxidored; I.
PROSITE; PS000290; IG MHC; 1.
PROSITE; PS000290; IG MHC; 1.
SEQUENCE 487 AA; 54402 MW; AFF16053590E6F68
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Q8TF03;
01-JUN-2002 (TYEMBLYEL 2
01-JUN-2002 (TYEMBLYEL 2
01-JUN-2003 (TYEMBLYEL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Homo sapiens (Human)
Eukaryota, Metazoa; Chordata,
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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Best Local S
Matches 209
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GO; GO:0006118; P:electron transport; II
InterPro; IPR003006; IG_MHC.
InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420 oxidored; I.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 456 AA; 50430 MW; C5F7C700
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Q8TDF3;
Q1-JUN-2002
Q1-JUN-2002
Q1-JUN-2003
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                 LARQLNEIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA
:| :|:|:|:||||:|||||:||
MALAMGFMPVDMGSLASAWEVEAMPLRLLPAWKVPTLLALGLFVCFYAYNFVRDVLQPYV
                          ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQ
                                                                                                 CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLMMAYQQVHANIENSWNEESVWRIEMY
                                                                                                                                                      QESONKFEKLÉVSVVNTTLÉCVÁYVLLSLVYLEGVLÁAÁLOLRRGTKYORFEDWLDHWLO
                                                                                                                                                                         RNQQSDFYKIFIBIVNKTLFIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ
                                                                                                                                                                                                                                                                                                                                  RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGFKDASRQVYICSNNIQARQQVIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIHIVDSDSSLAK--VPD-----EAPKVS--IIGSGDFARSLATRIVGSGFKVVVGSRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QESQNKFFKLPVSVVNTTLPCVAYVLLSLVYLPGVLAAALQLRRGTKYQRFPDWLDHWLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ
LSLGVLALGTLSLLAVTSLPSIANSLNWREFSFVQ
                                                                                                                                                                                                                                                                                                                                                                                         PKRTARLFPSAAQVTFQEEAVSSPEVIFVAVFREHYSSLCSLSDQLAGKILVDVSNPTEQ
                                                                                                                                                                                                                                                                                                                                                                                                            PKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSN--NM
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                                                                            HRKÓIGILSFFCAALHALYSFCLPLRRAHRYDLVNLÁVKQVLÁNKSHLW-VEEVWRMEIY
                                                                                                                                                                                                                                                                                                               EHLQHRESNAEYLASLFPTCTVVKAFNVISAWTLQAGPRDGNGQVPICGDQPEAKRAVSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.7%; Score 1074.5;
52.9%; Pred. No. 3.2e
tive 75; Mismatches
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Last annotation
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InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420 oxidored; I.
PROSITE; PS00024; HEMOPEXIN; 1.
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EMBL; AK040760; BAC30696.1; -.
GO; GO:0006118; P:electron transport;
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STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Strausberg R.;
Submitted (APR-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141
381
                                                                                                               321
                                                                                                                                                                                                                                                                          273 AGLLAAAYQLYYGTXYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMRRSERYL
                                                                                                                                                                                                                                                                                                                                                  201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 ALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLSSAREIENLPLRLFTLW 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 MHREHYDSLTELVDYLKGKVLVDVSNNRKINQYPESNAEYLAQLEPGAHVVKAFNTISAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
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                                                                                                                                                                                                                                                                                                                                            VCIFGTGDFGXSLGLKMLQCGYSIVFGSRNPQ-VSSLLPRGAEVLSYSEAASKSDIIILA
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FVQSKLGYLTLVLCTAHTLVYGGKRFLSPSILRWSLPSAYILALVIPCAVLV 432
                                                    FIQSTLGYVALLISTFHVLIYGWKRAFEEEXYRFYTPENFVLALVLESIVIL 444
                                                                                                               LRNATIT QALTNKDSPFITSYAWINDSYLALGILGFFLFLLLGITSLPSVSNMVNWREFR
                                                                                                                                              FLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWREFS 392
                                                                                                                                                                                                                      PGILAAILQLYRGTKYRRFPNWLDHWMLCRKQLGLVALGFAFLHVIYTLVIFIRYYVRWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALQSGTLDASRQVFVCGNDSXAKQRVMDIARTLGLTPLDQGSLMAASSIENYPLQLFPMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470 AA;
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Search completed: March Job time: 89 secs

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